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AAM40223 standard; protein; 229 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM40223;
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ID AAM4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
                                                                                                           March 25, 2006, 07:55:45; Search time 188 Seconds (without alignments) 535.201 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                              1 MAAQPLRHRSRCATPPRGDF.....LKSLMKILSEVTPDQSKPEN 229
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                          2443163
                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                               2443163 segs, 439378781 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                          - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           summaries
                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      geneseqp2000s:*
geneseqp2001s:*
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Maximum Match 100%
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1198
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Maximum DB seq length: 200000000
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Perfect score:
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Result No.	Score	Query	Length	DB	. OI	Description	
7	1198	100.0	229	4	AAM40223	Aam40203 Human nol	
7	1198	100.0	229	S	ABG34856		
m	1198	100.0	231	4	AAM42009	Human	
4	138.5	11.6	164	2	ABG34855	_	
ın	113	9.4	233	4	AAM93668	Human	
9	113	9.4	233	4	AAG93290	Human	
7	113	9.4	233	7	ADJ69163	Human	
80	113	9.4	233	œ	ADL31517		
σ	92	7.7	695	'n	ABB54167		
10	92	7.7	695	æ	ADS29356		
11	06	7.5	269	4	AA008972		
12	89	7.4	572	æ	ABM83354	Human	
13	88	7.4	623	4	AAB93182	Human	
14	89	7.4	623	Ŋ	ABB97233	Novel	
15	89	7.4	652	4	AAB93168	Human	
16	83	7.4	664	4	AAB83843	Amino	
17	89	7.4	664	4	AAB20219	Human	
18	88.5	7.4	388	œ	ADQ08702		
19	87.5	7.3	1245	7	ADC32818	Human	
20	86.5	7.2	470	60	ABM83305	Human	
21	86.5	7.2	699	9	ABU23878	Abu23878 Protein e	
. 22	98	7.2	158	7	ADH88711	_	
23	85.5	7.1	571	æ	ADU07910		
24	84.5	7.1	485	S	ABP51336		

Aab95788 Human pro			_	Aaw59461 Microbial	_	_	Aaw59458 Microbial	Aaw59459 Microbial	_		Aaw59464 Microbial	Aaw59496 Microbial		_	_	Abu23749 Protein e	Adx72944 Plant ful	Aav90242 Human cvc	Thale	-
AAB95788	ADC31196	AAU39678	ABM36197	AAW59461	AAW59463	AAW59457	AAW59458	AAW59459	AAW59462	AAW59460	AAW59464	AAW59496	AAP90110	AAW59456	AAW59465	ABU23749	ADX72944	AAY90242	ADN72405	AEA16977
4	7	4	9	~	~	~	~	0	~	~	7	7	Н	~	N	9	8	m	œ	6
496	496	479	479	598	598	598	598	598	598	598	598	599	909	607	607	663	278	325	493	493
7.0	7.0	7.0	7.0	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9
84	84	83.5	83.5	83	83	83	83	83	83	83	83	83	83	83	83	83	82.5	82.5	82.5	82.5
25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	45	43	44	45

## ALIGNMENTS

Wang D; Zhao QA; Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chrombolytic; drug screening; arthritis; inflammation; Ren F, Wa Zhang J, Qian XB, Yang Y, χ, Αζ, Ma X Liu C, Asundi V, Chen R, Wang Z, Wehrman T, Xu C, Goodrich R, Drmanac RT; Human polypeptide SEQ ID NO 3368. 23-DEC-1999; 99US-00471275.
21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
20-JUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-00653450.
14-SEP-2000; 2000US-00663191.
19-OCT-2000; 2000US-00663191. 26-DEC-2000; 2000WO-US034263 WPI; 2001-442253/47. (HYSE-) HYSEQ INC. WO200153312-A1. Homo sapiens. 26-JUL-2001. leukaemia. Tang YT,
Wang J, V 

N-PSDB; AAI59379

Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.

Claim 34; Fig 2; 201pp; English.

or ribozyme of 85P1B3.

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                                                    The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynuclectides are useful in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPF1 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALAGHFCLSSDKWCYLLKTKAIV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIV 180
                                                                                                                                                                                                                                                               Alzheimer's, Parkinson's disease, Huntington's disease, amyorrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression. Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and hrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                             system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGABEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 229;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cancer related protein encoded by cDNA 85P1B3.
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Pred. No. 9.7e-127;
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SEQ ID NO 3368; 10078pp; English.
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100.0%;
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N-PSDB; ABK70506.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AGEN-) AGENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 229 AA;
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Jakobovits A;
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   Example 5;
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ABG34856
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셤 δ 셤 Composition for modulating the status of 85P1B3 protein or a molecule comprising a substance e.g. antibody specific to, nucleic acid encoding,

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The invention relates to a composition comprising a substance that modulate the status of 85P1B3, where the status of a cell expresses modulate the status of 85P1B3, where the status of a cell expresses of modulate the status of 85P1B3, where the status of 65P1B3 gene product is modulated. Also included are a composition in the best of the 85P1B3 protein, in selected from an aa position having a value greater than 0.5 in the hydropathicity profile, an aa position having a value greater than 0.5 in the bydropathicity profile, an aa position having a value greater than 0.5 in the bydropathicity profile, an aa position having a value greater than 0.5 in the best of the 85P1B3 protein, a recombinate protein comprising the status profile, and position having a value greater than 0.5 in the best of the 85P1B3 protein, a recombinate protein comprising the status produces analobdy specific to the protein comprising the produces antibody specific to the protein, a single chain an integral produces antibody specific to the protein, a single chain heavy and monoclonal antibody specific to the protein, a single chain heavy and monoclonal antibody specific to the protein, a single chain heavy and monoclonal antibody specific to the protein, a single chain heavy and monoclonal antibody specific to the protein, a single chain heavy and monoclonal antibody specific to the protein, a single comprising a polymucleotide that encodes the WAD; inhibiting growth of cancer cells or treating the protein, antibody, polymucleotide to the protein, by administering the protein, antibody, polymucleotide to the protein of the protein, antibody specific to the protein, antibody specific to the protein and a cyclooxic agent conjugated to antibody and exposing the creating a mammalian immune response the chording a cyclooxic agent conjugated to antibody and conjugated to antibody and conjugated to antibody and expenses the protein, for generating a mammalian immune response directed to the protein, for generating a patient who bears cancer cel
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; Pred. No. 9.7e-127;
0; Mismatches 0;
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Best Local Similarity 100.
Matches 229; Conservative
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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer pertipheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                        nootropic; immunosuppressant;
                                                                                                                                                                                                                                                         Asundi V, Chen R,
Wehrman T, Xu C,
R, Drmanac RT;
        Human polypeptide SEQ ID NO 6940.
                                                                                                                                                                                2000US-00598042.
2000US-00620312.
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2000US-00552317
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Wang Z, Wehr
Goodrich R,
                                                                                                                                                                                                                                                                                             WPI; 2001-442253/47.
                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
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                                                                                                    WO200153312-A1
                                                                                    Homo sapiens.
                                                                                                                                    26-DEC-2000;
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                                                                                                                     26-JUL-2001.
                                                                   leukaemia.
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Wang J,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                Sxample
                        Human:
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Wang D; Zhao QA;

Ren F, Wa Zhang J,

Qian XB, Yang Y,

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encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzeimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries. The invention relates to human nucleic acids (AAIS7798-AAI61369) and the 2; SEQ ID NO 6940; 10078pp; English.

3 MAAQPLRHRSRCATPPRGDFCGGTBRAIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEEP MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEEP 100.0%; Score 1198; DB 4; Length 231; 100.0%; Pred. No. 9.8e-127; tive 0; Mismatches 0; Indels 0 229; Conservative Query Match Best Local Similarity Best Loca Matches 셤 ઠ

Sequence 231 AA;

.21 VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIV 180

AAGPOLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFL 120 

19 63

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62

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Composition for modulating the status of 85P1B3 protein or a molecule comprising a substance e.g. antibody specific to, nucleic acid encoding,
                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a composition comprising a substance that modulate the status of a cell expresses 85P1B3 gene product is modulated. Also included are a composition comprising a peptide region of 5 amino acids of the 85P1B3 protein, in
                                                                                                                                                                                                                                                                                                                  Challita-Eid P;
                                                                                                                                                                            Human; cytostatic; 85P1B3; cancer; immunogen; chromosome 15q14.
                              NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN 229
                                           NASEMDIQUVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN
                                                                                                                                                          Human cDNA 85P1B3 splice variant, open reading frame #3.
                                                                                                                                                                                                                                                                                                                  Ge ¥,
                                                                                                                                                                                                                                                                                                                  Afar D,
                                                                                                                                                                                                                                                                                                                                                                                                                 Example 38; Page 124; 201pp; English.
                                                                                                ABG34855 standard; protein; 164 AA.
                                                                                                                                                                                                                                                                                                                  Hubert RS,
                                                                                                                                                                                                                                                        28-AUG-2001; 2001WO-US026838.
                                                                                                                                                                                                                                                                            28-AUG-2000; 2000US-0228432P.
                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                  Faris M,
                                                                                                                                                                                                                                                                                                                                                                                              or ribozyme of 85P1B3.
                                                                                                                                                                                                                                                                                                                                             WPI; 2002-382963/41.
                                                                                                                                                                                                                                                                                              (AGEN-) AGENSYS INC.
                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABK70504,
                                                                                                                                                                                                                   WO200218578-A2.
                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                            Jakobovits A;
                                                                                                                                       15-JUL-2002
                                                                                                                                                                                                                                      07-MAR-2002
                                                                                                                   ABG34855;
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                                                 183
                                                                                                                                                                                                                                                                                                                  Raitano
                                                                                       ABG34855
                                                                             RESULT
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comprising a peptide region of 5 amino acids of the BSPIBB procein, in any whole number increment up to 229 that includes an as position any whole number increment up to 229 that includes an as position as elected from an aposition having a value less than 0.5 in the hydropathicity profile, an as position having a value greater than 0.5 in the percent accessible residue profile, an as a position having a value greater than 0.5 in the percent accessible residue profile, an as a position having a value greater than 0.5 in the beta-turn profile, or an as constition having a value greater than 0.5 in the beta-turn profile, as a position having a value greater than 0.5 in the beta-turn profile; a polynucleotide that encodes analogue peptide of 8, 9, 10 or 11 contiguous certaines of the BSPIBB protein; a recombinant protein comprising the annibody that binds to the BSPIBB protein; a antigen-binding region of a monoclonal antibody (MAD) that comprises the variable domains of the monoclonal antibody (MAD) that comprises the variable domains of the cancer calls or treating a perient who bears cancer calls that expresses the protein; and percein, and generating the protein; and percein antibody, polynucleotide concerned to the protein, by administering the protein antibody, polynucleotide and response the protein, and generating a mammalian immune response cribozyme that claeves the polynucleotide and relays that specifically recognize the protein, and generating a mammalian immune response directed to the protein, and generating a mammalian immune response an animunogenic portion of the protein or polynucleotide. The composition, which comprises an antibody specific to the protein, is useful for an immunogenic portion of the protein to a cell that expresses the protein by protein call that expresses the protein by protein call that expresses the protein by administering a call that expresses the protein by administering a call that expresses the protein by administering a cell that expresses the protein by administering

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length not form part of the invention. Note: The sequence data for this patent did format directly from EPO
to the antibody-agent conjugate. The methods are useful for inhibiting growth of cancer cells or treating a patient who bears cancer cells that expresses the protein, for generating a mammalian immune response directed to the protein, for detecting the presence of the protein or polynucleotide in a biological sample in a patient who has or who is suspected of having cancer and for monitoring 85PlB3 in a biological sample from a patient who has or who is sample from a patient who has or who is suspected of solutions. The gene for 85PlB3 is located on human chromosome 15q14. The present sequence is the 85PlB3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   830 Primers useful for synthesizing full length cDNA clones and their use
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T, Koga
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                                                                                                                                                                                                          DB 5; Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID NO 3550; 1380pp + Sequence Listing; English.
                                                                                                                                                                                                                                            1; Indels
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5, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; full length cDNA; cDNA synthesis; oligo-capping
                                                                                                                                                                                                                                                                              162 FCLSSDKWVCYLLKTKAIVNASEMDIONVPLSEKIAELK 200
                                                                                                                                                                                                                                                                                                 FFLSS-----YLLKTKAIVNASEMDIQNVPLSEKIAEVK 35
                                                                                                                                                                                                      11.6%; Score 138.5; DB 5 82.1%; Pred. No. 8.6e-07; ive 1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ai T, Hayashi K, Isi
Nagai K, Kojima S,
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                                                                                                                                                                                                                                                                                                                                                                                                  AAM93668 standard; protein; 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wakamatsu A, Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                            32; Conservative
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                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human polypeptide,
                                                                                                                                                                         Sequence 164 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1130094-A2
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                                                                                                                                                                                                        Query Match
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Sequence 233 AA

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-LSWVASQEDTNCILLRCVSCNVSVDKEQKLSKREKENGCVLETLCCAGCSLNLGTVYR 153
                                                                                                                                                           STHAALAALAALKGHPCLSSDKWCYLL--KTKAIVNASEMDIQNVPLSEKIABLKEKIVLTH 207
                                                                                                                                                                          95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a human protein. The human protein, preferably originated from tumour cell line, is applicable as a drug, a reagent for studying intracellular protein networks and a protein source for screening proteins for binding low molecular weight drugs. The human protein coding sequence is useful for gene diagnosis and gene therapy, expression vectors and transformant cells for detection of ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human protein originated from tumor cell line, applicable as drug, reagent for studying intracellular protein networks and protein source for drug screening, also encoded cDNA for gene diagnosis and gene
                                                                            ASMWSSMSEDASV----ADMERAQL--EREAAAAR-----ERPLVFLCSGCRRPLGDS
                                                                                                       VHLAWDLSR-SLGAVVFSRVTNNVVLBAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLY
                                                    31 ASFITSMEWDTQVVKGSSPLGPAGLGABEPAAGPQLPSWLQPERCAVFQCAQCHAVLADS
                         22;
9.4%; Score 113; DB 4; Length 233; 27.1%; Pred. No. 0.0011;
                          Indels
            Pred. No. 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                             AAG93290 standard; protein; 233 AA
                         30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000JP-00031062
2000JP-00034090
2000JP-00034091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-DEC-2000; 2000WO-JP008631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99JP-00346863
99JP-00346864
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2000JP-00071161
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                                                                                                                                                                                                                                                                                                                                                                                                                      Human; gene therapy; tumour
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                                                                                                                                                                                                                 208 NRLKSLMKILSE 219
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                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Human protein HP10650
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N-PSDB; AAH68575.
            Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eguchi C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200142302-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-DEC-1999;
06-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                  13-SEP-2001
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Length 233; 88; Indels

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present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with alterred mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial recephalopathy lactic acidosis and stroke (MELAS), myocionic epilepsy ragged red fibre syndrome (MERRP) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence.is a human heart mitochondrial protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 VHLAWDLSR-SLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLY 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 CTPKNLDYKRDLFCLSVEAIESYVLGSSEKQIV-SEDKELFNL---ESRVEIEKSLTQME 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 STHAALAALAGHFCLSSDKMVCYLL--KTKAIVNASEMDIQNVPLSEKIAELKEKIVLTH 207
                                                                                                                                                                                                                                                                                                                                                                    31 ASFTTSMEWDTQVVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAVLADS 90
                                                                                                                                                                                                                                                                                                                                                                                                       49 ASMWSSMSEDASV----ADMERAQL--BEEAAAAB-----BRPLVFLCSGCRRPLGDS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oligonucleotide primers (830 cDNAs) useful for synthesizing full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human; medicine; signal transduction; glycoprotein; transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human protein encoded by a full length cDNA clone SeqID 3550.
                                                                                                                                                                                                                                                                           / Match 9'4%; Score 113; DB 7;
Local Similarity 27.1%; Pred. No. 0.0011;
les 52; Conservative 30; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashi K,
K, Kojima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; SEQ ID NO 3550; 1340pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADL31517 standard; protein; 233 AA.
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183865.
07-JUL-2000; 2000EP-00114089.
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su A, Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 NRLKSLMKILSE 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oligo-capping method
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                                                                                                                                                                                                                                     Sequence 233 AA;
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ADL31517
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                                                                                                                                                                                                                                                                                                                       154 CTPKNLDYKRDLFCLSVEAIESYVLGSSEKQIV-SEDKELFNL---ESRVEIEKSLTQME 209
                                                                                                                                                                                                                                                    --LSWVASQEDTNCILLRCVSCNVSVDKEQKLSKREKENGCVLETLCCAGCSLNLGYVYR 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Huntington's disease; osteoarthritis;
Leber's hereditary optic neuropathy; LHON;
mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
osteopathic; ophthalmological; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating
                                                                                                                        31 ASFITISMENDIOVVKGSSPLGPAGLGAREPAAGPQLPSWLQPERCAVFQCAQCHAVLADS
                                                                                                                                                                  49 ASMWSSWSEDASV----ADMERAQL--EBERAAAR-----ERPLVFLCSGCRRPLGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to novel mitochondrial targets that can be used
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human heat mitochondrial protein as a therapeutic target SegID969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glenn GM;
                                                                                    22;
                                            Length 233;
                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mitochondrial; human; screening assay; diabetes mellitus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Taylor SW,
                                                                                88;
                                   Query Match 9.4%; Score 113; DB 4; Best Local Similarity 27.1%; Pred. No. 0.0011; Matches 52; Conservative 30; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gibson BW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 969; 180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ69163 standard; protein; 233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          m,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-APR-2002; 2002US-0372843P.
17-JUN-2002; 2002US-0389987P.
20-SBP-2002; 2002US-0412418P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-APR-2003; 2003WO-US010870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 208 NRLKSLMKILSE 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BUCK-) BUCK INST AGE RES.
                                                                                                                                                                                                                                                                                                                                                                                                              : ||:|
210 DVLKALQMKLWE 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-845369/78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fahy ED,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the disease.
  Sequence 233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003087768-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MITO-) MITOKOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Warnock DE;
                                                                                                                                                                                                                                                    96
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RESULT ADJ6916

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Ishii S, Kawai Y; S, Otsuki T, Koga H;

Ghosh

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8;
This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polypeptide sequence is a full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research
                                                                                                                                                                                                                                                                                                                                             91 VHLAWDLSR-SLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLY 149
                                                                                                                                                                                                                                                                                                                                                                   CTPKNLDYKRDLFCLSVEAIESYVLGSSEKQIV-SEDKELFNL---ESRVEIEKSLTQME 209
                                                                                                                                                                                                                                                                                                                                                                                                                  STHAALAALAALKGHFCLSSDKWVCYLL--KTKAIVNASEMDIQNVPLSEKIAELKEKIVLTH 207
                                                                                                                                                                                                                                                                             31 ASPTTSMEWDTQVVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAVLADS 90
                                                                                                                                                                                                                                                                                                             95
                                                                                                                                                                                                                                                                                                 | | : | | | | : : | | | | | | | | ASMWSSMSEDASV----BDMERAQL--BEBAAAAB-----ERPLVFLCSGCRRPLGDS
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleotide sequence useful in the identification or Lactococcus lactis and related species.
                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
                                                                                                                                                                                                         9.4%; Score 113; DB 8; Length 233; 27.1%; Pred. No. 0.0011;
                                                                                                                                                                                                                                           88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SD;
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                                                                                                                                                                                                                                         30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; SEQ ID NO 869; 2504pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INRG ) INRA INST NAT RECH AGRONOMIQUE
                                                                                                                                      length human protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Renault P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABBS4167 standard; protein; 695 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lactococcus lactis protein yihC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-APR-2000; 2000FR-00004630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-APR-2000; 2000FR-00004630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lactococcus lactis; IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NRLKSLMKILSE 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVLKALOMKLWE 221
                                                                                                                                                                                                                                           52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-043418/06
                                                                                                                                                                                                                           Similarity
                                                                                                                                                                        Sequence 233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FR2807446-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    154
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                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                             HMGMNFWFELATLIVIMLIGHLIEMKAIMGAGDALKDLASLVPKKAHLKSGKDVELSELK 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a
                  equivalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cold tolerance, heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                             101 LGAVVESRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRG
                                                                                                                                                               Gaps
in lactic bacteria, particularly useful in the production of yogurt cheese. Note: The sequence data for this patent is based on equivale patent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp. wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                               34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant DNA construct; transformed plant; improved plant
                                                                                                                                  Length 695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goldman BS
                                                                                                                                                             20;
                                                                                                                                  DB 5;
                                                                                                                                  Score 92; DB 5
Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                            IABLKEKIVLTHNRLKSLMKILSEVTPDQS 225
                                                                                                                                                             28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 18389; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen X,
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                                                                                                                                                                                                                                                                                                                                                                                                               standard; protein; 695
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                                                                                                                                  7.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacterial polypeptide #18389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-FEB-2002; 2002US-0360039P
                                                                                                                                               Local Similarity 25.3%
les 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HINKLE G J.
SLATER S C.
CHEN X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-061375/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hinkle GJ,
                                                                                                      Sequence 695 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS2003233675-A1
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                                                                                                                                                                                                                                                                                                                                                                                                               ADS29356
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADS29356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria.
                                                                                                                                  Query Match
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(CHEN/)
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                                                                                                                                                               Matches
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comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant is a crop plant such as maize or soybean. The method of producing a transformed plant to such as maize or soybean. The method of producing a transformed plant to having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polymucleotide or polypeptide is useful for improving plant properties.

The recombinant DNA construct is useful for improving plants with compressed plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme sometic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the content, improved yield by modified seed oil or protein yield and/or content, improved yield by modification of farbchydrate, nitrogen or phosphorus use and/or uptake, by modification of phosphorus use and/or uptake, by modification of phosphorus conting improved light production or improved galactonannan condition, may not be seed on the printed specification but was obtained in electronic form part of the printed specification but was obtained in electronic condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 IGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNLLPCGSCGIPVGFHLYSTHAALAALRG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 HF------CLSSDKMVCYLLKTKAIVNASE--MDI------QNVPLSE-K 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 HMGMNFWFELATLIVIMLIGHLIEMKAIMGAGDALKDLASLVPKKAHLKSGKDVELSELK 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; architits; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.7%; Score 92; DB 8; Length 695; 25.3%; Pred. No. 1:5; ive 28; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 IAELKEKIVLTHNRLKSLMKILSEVTPDQS 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAO08972 standard; protein; 269 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-2001; 2001WO-US004927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38; Conservative
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N-PSDB; AAI88903.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 695 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200164835-A2
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AAO0897
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                             lated nucleic acids and polypeptides, useful for preventing diagnosing treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                            The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymetides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, insue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 PMPDRRAEREQDPRVAPQ-------QCAVC---LQPFCHLYWGCTRTGCYGCLA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTY-NLLFCGSCGIPVGFHLYSTHA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 PFCELNLGDKCLDGVLNNNSYESDILKNYLAT-RGLTWKNML-------TES 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 YRRQAAQPPH---CPAPEGEPGAPQALGDAPSTSVSLTTAVQDYVCPLQGSHALCTCCFQ 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 HRSRCATPPRGDFC-----GGTERAIDQA----SFTTSMEWDTQVVKGSSPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy; human diagnostic and therapeutic polynucleotide; dithp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shen F;
J, Elder LV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wright RJ, Bruns CM, Marjanovic MM, Shen F;
TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV
Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin
Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---GPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74;
                                                                                                                                    20; SEQ ID NO 22864; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALAALRGHFCLS----SDKMVCYLLKTKAIVNASEMDIQNVPLSE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 LMALQRGVFLLSDYRVTGDTVLCYCCGLRSFRELTYQYRQNIPASE 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 269;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.5%; Score 90; DB 4;
23.0%; Pred. No. 0.58;
tive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABM83354 standard; protein; 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-SEP-2003; 2003WO-US028227.
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12-SEP-2002; 2002US-0410260P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 23.0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004023973-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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Peralta CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schmidt JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mooney EM,
                                 Isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABM83354;
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                                                                                                                                    Claim
                                                                      and
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ID ABM
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Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length

Yamamoto J;

Saito K, Ya Otsuki T;

Isogai T, Nishikawa T, Hayashi K, S Sugiyama T, Wakamatsu A, Nagai K,

WPI; 2001-318749/34.

Ishii S,

(HELI-) HELIX RES INST

99JP-00300253. 2000JP-00118776. 2000JP-00183767 2000JP-00241899

27-AUG-1999; 11-JAN-2000; 02-MAY-2000; 09-JUN-2000;

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The invention relates to novel diagnostic and therapeutic polymucleotides selected from one of the 2722 sequences defined in the specification. A puricleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polymuclootides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine disorder, neurological disorder, developmental disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp infections caused by virus, bacteria, fungi or parasite. The dithp infections and also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline consention. Note: The sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       399 PMPDRRAEREQDPRVAPQ------QCAVC---LQPFCHLYWGCTRTGCYGCLA 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----SLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTY-NLLFCGSCGIPVGFHLYSTHA 153
                                                                                                                          New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnostic a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 HRSRCATPPRGDFC-----GGTERAIDQA----SFTTSMEWDTQVVKGSSPL----
Vitt UA, Kirton ES;
Jackson JL, Gietze
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---GPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 ALAALRGHFCLS----SDKMVCYLLKTKAIVNASEMDIQNVPLSE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.4%; Score 89; DB 8; Length 572;
23.0%; Pred. No. 2.4;
ive 26; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             443 PFCELNIGDKCLDGVLNNSYESDILKNYLAT-RGLTWKNML-----
Spiro PA, Stewart EA, Wingrove J,
3 M, Policky JL, Hurwitz BL, Ma Y,
Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human protein sequence SEQ ID NO:12128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB93182 standard; protein; 623 AA
                                                                                                                                                                                                                     Claim 27; Page; 190pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.0%;
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                                                                       WPI; 2004-329368/30.
         Kwong M, Fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 572 AA;
                                                                                       N-PSDB; ACN42006
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Lagace RE,
Xu Y, Kwor
                                    Patury S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches
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the 5-end sequence/3-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length AAH13613 to AAH13612 represent human capit sequences; AAB32446 to AAB35893 represent human amino acid sequences, and AAH13629 to AAH13612 represent oligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes primer sets for synthesising 5602 full-length CDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oplynucleotide comprises at least 15 nucleotides and the combination of oligonucleotide comprises at least 15 nucleotides and the combination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 ----SLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTY-NLLFCGSCGIPVGFHLYSTHA 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 HRSRCATPPRGDFC-----GGTERAIDQA-----SFTTSMEWDTQVVKGSSPL
                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; SEQ ID NO 12128; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 ALAALRGHFCLS----SDKMVCYLLKTKAIVNASEMDIQNVPLSE 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Length 623;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.4%; Score 89; DB 4
23.0%; Pred. No. 2.7;
ive 26; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 623 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51
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Matches
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ID ABB
XX
AC ABB
g
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28-JUL-2000; 2000EP-00116126

Homo sapiens EP1074617-A2 us-09-942-052a-728.rag

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Human; primer; detection; diagnosis; antisense therapy; gene therapy.
          protein sequence SEQ ID NO:12100.
                                                        Homo sapiens
                                                                                                                                                                                                                                                     Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51
                                                                                                                                                                                                                                          Ota T,
             Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTB). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anamia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----SLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTY-NLLFCGSCGIPVGFHLYSTHA 153
                                                      antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy; neuroprotective; antiparkinsonian; protein therapy; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----òcavc---Loppechiywgcirrgcygcla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 HRSRCATPPRGDFC-----GGTERAIDQA-----SFTTSMEWDTQVVKGSSPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                              An isolated polynucleotide for treating diseases associated with its encoded polypeptide such as cancer and multiple sclerosis.
                                           antiinflammatory; immunomodulator;
                                                                                                                                                                                                                                          Ren F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---GPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 ALAALRGHFCLS--'--SDKMVCYLLKTKAIVNASEMDIQNVPLSE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  538 LVÁLORGVFLLSDYRVTGÖTVLCYCCGLRSFRELTYOYOONIPASE 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.4%; Score 89; DB 5; Length 623;
                                                                                                                                                                                                                                          Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.0%; Pred. No. 2.7; tive 26; Mismatches
                                                                                                                                                                                                                                                    Drmanac RT;
                                                                                                                                                                                                                                                                                                                                               Example 2; SEQ ID NO 501; 509pp; English.
                                                                                                                                                                                                                                         Asundi V,
                    Novel human protein SEQ ID NO: 501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB93168 standard; protein; 652 AA.
                                                                                                                                                                                                                                                                                                            isolated polynucleotide for
                                            antianaemic; vulnerary;
                                                                                                                                                                                                                                         Liu C, Zhou P, As
Yang Y, Wehrman T,
                                                                                                                                                                     10-SEP-2001; 2001WO-US026015.
                                                                                                                                                                                            11-SEP-2000; 2000US-00659671
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450 PMPDRRAEREQDPRVAPQ-
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 23.0
Matches 52; Conservative
                                                                             expressed sequence tag
                                                                                                                                                                                                                                                                        WPI; 2002-292408/33.
                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                        N-PSDB; ABN32419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 623 AA;
                                                                                                                        WO200222660-A2
                                                                                                   Homo sapiens
                                                                                                                                               21-MAR-2002
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                                                                                                                                                                                                                                       Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                      Xue AJ,
                                            Human;
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(first entry)

26-JUN-2001

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length CDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polyuncleotide which comprises one of the 5602 mucleotide sequences defined in the specification, where the cultionide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of a noligonucleotide comprising a sequence complementary to the complementary strand of a polyuncleotide which comprises a 3'-end sequence and an oligonucleotide which comprises a 3'-end sequence complementary to a complementary strand of a polyuncleotide which comprises a 1'-end sequence, where the comprises a 1'-end sequence, where the comprises a 1'-end sequence, where the comprises a 1'-end sequence of specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primer sets of the primers are useful for synthesising polynucleotides, carricularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AAH33166 to AAH3828 and AAH33631 to AAH38218 contains the complements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonuclectides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes primer sets for synthesising 5602 full-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --TES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; SEQ ID NO 12100; 2537pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oggai T, Nishikawa T, Hayashi K, Saito K, Ye
Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
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                                                                                                                                                                                                                        11-JAN-2000; 2000JP-00100253.
02-MAY-2000; 2000JP-001183767.
09-JUN-2000; 2000JP-00183767.
                                                                                                                                            28-JUL-2000; 2000EP-00116126
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Best Local Similarity 23.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                     (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isogai T,
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EP1074617-A2
                                                                                                                                                                                                                29-JUL-1999;
                                                                        07-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           479
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Search completed: March 25, 2006, 07:59:14 Job time : 191 secs

GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

March 25, 2006, 07:59:30 ; Search time 40 Seconds
(without alignments)
550.841 Million cell updates/sec

US-09-942-052A-728 Title: Perfect score:

1 MAAQPLRHRSRCATPPRGDF.....LKSLMKILSEVTPDQSKPEN 229 Sequence:

Scoring table:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	CODDET-TO-THE CO	probable phosphori	hypothetical prote	kanamycin kinase (	NAD-dependent DNA	dlutamate synthase	ferrichrome bindin	DNA ligase (NAD de	formate hydrogenly	sugar transporter	DNA polymerase I	transport protein.	glucuronide permea	glucuronide permea		~	ĽΩ	hypothetical prote	receptor kinase-li	protein-tyrosine-p	IME2-dependent sig	aminon	probable aminometh	GTP-binding protei	late competence op	probable hydroxyme	UL104 protein - hu	UDP-3-0-3-hvdroxvm	hypothetical prote
SUMMARIES	ID	C86731	D71293	T46399	A43623	A97229	JQ1977	AE2074	D97047	B69099	A85433	F87678	D90404	H85767	C90919	B64918	T41977	T44221	S40764	B85440	A55148	855167	H90789	C85650	C86823	F83816	F86484	OQBEK3	H82098	T44036
	DB	7	~	7	7	7	-	7	7	~	~	7	7	7	~	7	~	~	N	~	٦,	7	7	7	7	7	7	-	7	7
	Query Match Length	695	597	306	250	699	2194	361	663	143	493	296	329	457	457	457	640	662	1418	996	1711	469	386	386	437	188	578	o	351	·
*	Query	7.7	7.6	7.4	7.3	7.2	7.1	7.1	6.9	6.9	6.9	6.9	6.8	6.8	6.8	6.9	6.8	6.8	6.8	6.7	6.7	6.7	٠	٠	•	•		9.9	6.5	6.5
	Score	92	90.5	89	8	86.5	82	84.5	83	82.5	82.5	82	81.5	81.5	81.5	81.5	81.5	81.5	81		80.5	80	79	79	79	78.5	78.5	78.5	78	77.5
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30 77.5 6.5 1013 2 T31211 31 77.5 6.5 1643 2 T14274 33 77 6.4 381 2 AD1113 34 77 6.4 721 2 F87611 35 76.5 6.4 307 2 AG2017 36 76.5 6.4 387 2 D69392 37 76.5 6.4 387 2 D69392 38 76.5 6.4 764 2 H98143 39 76.5 6.4 764 2 H98143 40 76.5 6.4 1554 2 AD3144 76.5 6.4 1554 2 AD3164 41 76.5 6.3 310 2 A55053 43 75.5 6.3 415 2 T46716 44 75.5 6.3 1534 2 S59604	trwC protein homol	versican precursor	hypothetical prote	TonB-dependent rec	melanotransferrin	glycerol-3-phospha	probable acv1-CoA	cellulase - Fibrob	chbBc protein (1160	formate dehydrogen	probable DNA (cyto	glycerol dehydroge	endothelial monocy	hypothetical profe	probable UvrD - Mv	DNA (cytosine-5-)-
លលលលលលលលលលល លល់ លំលំងងងងងងងងងងងយ៉េយ៉េយ៉េយ៉េ	T31211	T14274	AD1113	F87611	TFHUM	AG2017	D69392	S57526	H98143	AD3144	T06370	AH0936	A55053	T46716	D70951	S59604
លលលលលលលលលលល លល់ លំលំងងងងងងងងងងងយ៉េយ៉េយ៉េយ៉េ	0	~	~	~	Н	N	N	N	~	~	~	7	~	~	~	~
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0 11 2	77.5	77.5	77	77	77	76.5	76.5	76.5	76.5	76.5	76.5	92	75.5	75.5	75.5	75.5
	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

5	731
5	1

Copper-potassium transporting ATPase B copB [imported] - Lactococcus lactis subsp. lac.
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Species: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004
C;Accession: C86731
A;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Bhr.
Genome Res. 11, 731-753, 2001
A;Reference number: A66625; MUD:21235186; PMID:11337471
A;Reference number: A66625; MUD:21235186; PMID:11337471
A;Residues: C86731
A;Residues: 1-695 cSTO>
A;Residues: 1-695 cSTO>
A;Cross-references: UNIPROT:Q9CH87; UNIPARC:UPI00000C6919; GB:AE005176; PID:g12723778;
A;Experimental source: strain IL1403
C;Genetics:
A;Genetics:
A;Gene

Gaps 34; 7.7%; Score 92; DB 2; Length 695; 25.3%; Pred. No. 2; iive 28; Mismatches 50; Indels Query Match Best Local Similarity 25.3\* Matches 38; Conservative

101 LGAVVESRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRG 160 Š

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161 HF------CLSSDKWVCYLLKTKAIVNASE--MDI------QNVPLSE-K 195 à 셤

196 IAELKEKIVLTHNRLKSLMKILSEVTPDQS 225 ò

::| ::| |:| |:| |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| 유

RESULT 2

probable phosphoribosylglycinamide formyltransferase - syphilis spirochete C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C;Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004

C;Accession: D71293
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete. A;Reference number: A71250; MUID:98332770; PMID:965876

A,Accession: D71293 A,Status: preliminary; nucleic acid sequence not shown; translation not shown A,Molecule type: DNA

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A, Accession: A43623
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-250 <TEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-669 < KUR>
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                                NID
                         A;Cross-references: UNIPROT:083693; UNIPARC:UPI00000D3290; GB:AE001243; GB:AE000520; A;Experimental source: strain Nichols C;Genetics: A;Genetics: TP0695
                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                 54 GLGABEPAAGPQLPSWLQP-ERCAVFQC--AQCHAVLADSVHLAWDLSRSLGAVVFSRVT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 NNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKWV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 GRVIIE-BFIVGREFSLEG----LIFDGT------LYVT--ALA-----DRHI 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein DKFZp434N2420.1 - human (fragment)
C.Species: Home sapiens (man)
C.Species: Home sapiens (man)
C.Species: Home sapiens (man)
C.Species: 104-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C.Accession: T46399
R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000
A.Reference number: Z23031
A.Accession: T46399
A.Accession: T46399
A.Accession: T46399
A.Accession: T46399
A.Accession: J306 AAAA
A.Residues: J-306 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----SLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTY-NLLFCGSCGIPVGFHLYSTHA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66
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C;Species: Campylobacter jejuni
C;Species: Peb-1993 #sequence_revision 11-Feb-1993 #text_change 31-Dec-2004
C;Accession: A43623
R;Tenover, F.C.; Gilbert, T.; O'Hara, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Homo sapiens (man)
Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                -----TSMEWDTQVVKGSSPLGPA
                                                                                                                                                                                                                                                                                                                                                                90 CALP--GHRLEATKNATDKTRMRACFTRARLRCPRFTFLEPDSFAWDT-----PPGHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---GPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSR-----
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 HRSRCATPPRGDFC-----GGTERAIDQA-----SFTTSMEWDTQVVKGSSPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74;
                                                                                                                                                                                                                                                  65;
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28.0%; Pred. No. 2.2;
iive 19; Mismatches 47; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 RLCSHLHSAGLSPPLVVKPTDNMGARGCTLAOCKDTLINACAVARQFSRS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 ALAALRGHFCLS----SDKWVCYLLKTKAIVNASEMDIQNVPLSE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.4%; Score 0.,
23.0%; Pred. No. 1.3;
+ive 26; Mismatches
                                                                                                                                                                                                                                                                                                         12 CATPPRGDFCGGTERAID----QASFT-----
                                                                                                                                                                                                                                                  51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52; Conservative
                                                                                                                                                                                                        Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
A;Residues: 1-597 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:
CF 227
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                                                                                                                                                                                     Query Match
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Matches 5
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Plasmid 22, 52-58, 1989
A;Title: Nucleotide sequence of a novel kanamycin resistance gene, aphA-7, from Campylc
A;Reference number: A43623; MUID:89387451; PMID:2550983
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                                                                                                                                                                                                       A;Cross-references: UNIPROT:P14508; UNIPARC:UP1000012DEBC; GB:M29953; GB:J03316; NID:g1
C;Superfamily: aminoglycoside 3'-phosphotransferase (kanamycin kinase)
C;Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1 A;Reference number: A96900; MUID:21359325; PMID:21359325 A;Accession: A97229 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GB: AE001437; PIDN: AAK80620.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R.; Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C, Accession: A97229
C, Accession: A97229
R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 VPSRVTNNVVLEAPPLVGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRG-HFC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 IFSKTTYSVKREAEMMMLSDKLKVPDV-----IEYGVREHSEYLIMSELRGKHID 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAD-dependent DNA ligase [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 31-Dec-2004
C;Acession: A97229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 DLSR----SLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNL-----LFCGSCGIPVGF
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CFIDHPIKYI---ECLVNALHQLQAIDIRNCPFSSKIDVRLKELKYLLDNRIADI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 LSSDKMVCYLLKTKAIVNA----SEMDIQNVPLSEKI-AELKEKIVLTHNRLKSL 213
                                                                                                                                                                                                                                                                                                                                                                                              18;
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                                                                                                                                                                                                                                                                                                                            DB 2; Length 250;
1.3;
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                                                                                                                                                                                                                                                                                                                                                                                        46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                               Score 88; DB : Pred. No. 1.3; 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.2%; Score 86.5; Di
27.4%; Pred. No. 6.2;
Live 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: CAC2673
C,Superfamily: DNA ligase (NAD), LigA type
                                                                                                                                                                                                                                                                                                                                  7.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNIKSISDLYRITKE 480
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                                                                                                                                                                                                                                                                                                                            Query Match 7.3% Best Local Similarity 28.7% Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.2% Best Local Similarity 27.4% Matches 37; Conservative
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A;Molecule_type: DNA
A;Residues: 1-143 <MTH>
A;Cross-references: UNIPROT:O27769; UNIPARC:UPI000066781; GB:AE000929; GB:AE000666; N1
A;Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               formate hydrogenlyase, iron-sulfur subunit 2 - Methanobacterium thermoautotrophicum (si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: B69099
S; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.R.; Doucette-Stamm, L.A.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, P. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funk A; Reference number: A69000; MUID:98037514; PMID:9371463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: B69099
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: nrfC protein; ferredoxin 2{4Fe-48} homology
F;62-118/Domain: ferredoxin 2{4Fe-48} homology <FER2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 PERCAVFOCAQCHAVLADSVHLAWDLSRSLGAVVF--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    468 YRITKB 473
                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-663 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C. Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               요
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                                         Gerichtome binding protein of ABC transporter all2147 [imported] - Nostoc sp. (strain F G;Species: Nostoc sp. PCC 7120
G;Species: Nostoc sp. PCC 7120
G;Becies: Nostoc sp. pcC 7120
G;Becies: Nostoc sp. etrain PCC 7120
G;Becies: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
G;Accession: AB2074
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Matanabe, A.; Iriguchi DNA Ras. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUD:21595285; PMID:11759840
A;Status; preliminary
'Molecule type: mRNA
Residues: 1-2194 «GRE»
Cross-references: UNIPROT:Q03460; UNIPARC:UP1000012B7FA; GB:L01660; NID:g166411; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:O8YV34; UNIPARC:UPI00000CE32E; GB:BA000019; PIDN:BAB73846.1;
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1037 BPLADGSR--NPKRS-----AIKQVASGRFGVSSYYLTNADELQIKMAQGAKP---- 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1083 GEGGELPGHKVIGDIAITRNSTAGVGLIS--PPPHHDIYS-----IEDLAQLIHDLKN 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -SCGIPVG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----FITSMEWDTQVVKGSSPLGPA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --SD----LLADVPVVG----NIGNOPSLEKILSLKPDLI 163
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 FHLYSTHAALAA--LRGHPCLSSDKMVCYLLKT-----KAIVNASEMDIQNVPL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.1%; Score 84.5; DB 2; Length 361; 26.1%; Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                         Query Match
7.1%; Score 85; DB 1; Length 2194;
Best Local Similarity 24.7%; Pred. No. 39;
Matches 58; Conservative 22; Mismatches 79; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Genetics:
A,Gene: all2147
C,Superfamily: ferrichrome-iron transport protein fecB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 SLGAVVPSRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 OPLRHRSRCATPPRGDFCGGTERAIDQAS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 LTHNRLKSLMKILSEVTP 222
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Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-361 < KUR>
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-SRVTNNVVLEAPFLVGIEG 125

25;

Indels

99 DB 2;

26; Mismatches

Length 143;

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DNA ligase (NAD dependent), LigA [imported] - Clostridium acetobutylicum C;Species Clostridium acetobutylicum C;Species Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 31-Dec-2004 C;Accession: D97047 Exeton, G;Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Le Sholling, J.; Breton, G;Omelchenko, M.V.; Smith, D.R. Jacteriol. 183, 4823-4838, 2001 Exeton, Grapt Sequence and Comparative Analysis of the Solvent-Producing Bacterium C A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q97JS8; UNIPARC:UPI0000CA10F; GB:AB001437; PIDN:AAK79167.
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---- LFCGSCGIPVGFHLYSTHAAL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 AALRGHFCLSSDKMVCYLLKTKAIVNASEMDIQNVP-LSEKIAE-LKEKIVLTHNRLKSL 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 GAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.9%; Score 83; DB 28.6%; Pred. No. 13; ative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Gene: CAC1195
C,Superfamily: DNA ligase (NAD), LigA type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 28.6%
Matches 36; Conservative
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C;Species: Sulfolobus solfataricus
C;Species: 4-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: D90404
R;She, Q; Singh, R.K.; Confalonieri, F; Zivanovic, Y.; Allard, G; Awayez, M.J.; Char Jong, I.; Jeffrise, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Reference number: A99139
A;Accession: D90404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross_references: UNIPROT:Q97W97; UNIPARC:UPI0000646FA; GB:AE006641; NID:g13815639; C;Genetics:
A;Gene: SSO2338
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Y. Petra, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe iller, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodace Nature 409, 529-533, 2001

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Bscherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116
                                                                      271 CDTPLPQPLDALTVREPÜKEALAAFLEQMEFRSLARRVGDGSAAATPGTL--DRPAAPPK 328
                                                                                                                                         LP----SWL-----QPERC--AVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSR 108
                                                                                                                                                                                                     329 APVVSVSYMGAAARAAAHPVEPVKIDHAAYACVRDLATLKAWVAKATD----KGLVAFDT 384
                                                                                                                                                                                                                                                                                                                                        ---SLAIAPGEACYIP-- 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 APFLVG------IEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - SYVAYYLLKNWNVINISGILIMLIALFELNGKEFGERSKISVSFPRLTSILIYVSALTP 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 CATPPRGDFCGGTERAIDQ---ASFTTSMEWDT---QVVKGSSPLGPAGLGAEEPAAGPQ
                                                                                                                                                                                                                                                                     109 VTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDK
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C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transport protein, probable [imported] - Sulfolobus solfataricus
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A;Cross-references: UNIPROT:Q8X673; UNIPARC:UP1000000BE5;
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 VRFLVGVIFGLLTSYAVESAVKSGRNVLVGFTTAGWPIGWVI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47;
                                                                                                                                                                                                                                                                                                                                        385 BTD-----ALSSAT----AGLCGV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 MVCYLLKTKAIVNASEMDIQNVPLSEKIAELK 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.8%; Score 81.5; DE 22.2%; Pred. No. 7.4; tive 30; Mismatches
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Best Local Similarity
Matches 40; Conserva
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A; Residues: 1-329 < KUR>
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                          Gigeries: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: A85433
F;Ancession: A85433
F;Ancession: A85435
F;Ancession: A85435
F;Ancession: A85435
F;Ancession: A85435
F;Ancession: A85435
F;Ancession: A85001; MUD:20083488; PMID:10617198
F;Aritle: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
F;Areference number: A85001; MUD:20083488; PMID:10617198
F;Areference and A85433
F;Areferences: UNIPROT:023213; UNIPARC:UPI000009F22F; GB:NC_001268; NID:g7270615; ECGenetics:
F;Cenetics:
F;Cenetics
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C;Species: Caulobacter creacentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
R;Micrann, W.C; Feldblyum, T.V; Paulsen, I.T; Nelson, K.E; Eisen, J.; Heidelberg, J.
B; Laub, M.T; DeBoy, R.T; Dodson, R.J; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A;Title: Complete Genome Sequence of Caulobacter creecentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q9A2U2; UNIPARC:UPI00000C7AB1; GB:AE005673; NID:g13425184; C;Genetics:
C;Genetics:
A;Gene: CC3464
C;Superfamily: DNA-directed DNA polymerase I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
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   AVVILEDRCIGCGLCRDACPVG--AITLNERGVAVKCDLCIDRDKPLCVMVCPKGALSES 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QCAQCHAVLADSVHLAWDLSRSLGAVVF---SRVTNNVVLEAPFLVGI------EGSLK- 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 GRISDIIGRRYTIVLASILFMLGSILMGWGPNYPVLLSGRCTAGLGVGFALMVAPVYSAE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 AALAALKG-----HFCLSSDKWVCYLLK---TKAIVNAS---EMDIQNVP---LSEKIA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OCAIVASIV--SIIFGYDTGVMSGAMVFIEEDLKTNDVQIEV--LTGILNLCALVGSLLA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 493;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymerase I [imported] - Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
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KMPESPRWLIMQGRLKEGKEILELVSNSPEEAE 227
                                                                   184 EMDIQNVPLSEKIAELKEKIVLTHNRLKSLMK 215
                                                                                                         SEDM------MAAKRDKIAGELKRLKNIMK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.9%; Score 82.5; Dilarity 24.9%; Pred. No. 10; Conservative 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.8%; Score 82; DB
.larity 24.1%; Pred. No. 26;
Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
Les 53; Conserv
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A;Molecule type: DNA
A;Residues: 1-967 <STO>
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Local Sim.
51;
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Best Local S
Matches 53
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Best Local S
Matches 51
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7;

27;

Mismatches

DB 2; Length 457; 53; Indels

#status predicted <TM03

#status predicted

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95 WDLSRSLGAVVFSRVTNNV-----VLEA-----PFLVGIEGSLKGSTYNLL-FCGSCG 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;231-247/Domain: transmembrane #status predicted <TMO5>F;263-279/Domain: transmembrane #status predicted <TMO6>F;310-326/Domain: transmembrane #status predicted <TMO7>F;408-424/Domain: transmembrane #status predicted <TMO8>
                                                                                                                                                       C, Keywords: carrier protein, transmembrane protein F;37-53/Domain: transmembrane #status predicted <TMO1>F;81-97/Domain: transmembrane #status predicted <TMO2>
                   A; Experimental source: strain, K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.8%; Score 81.5;
25.2%; Pred. No. 11
tive 30; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIAELKEKIVLTHNRLKSLMKILSEVT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K--KFKEIVVEIDNRKKVQQQLISDIT 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            completed: March 25, 2006, 08:03:57.
                                                                                                                            melibiose carrier
                                                                                                                                                                                                                                                                       F;152-168/Domain: transmembrane F;184-200/Domain: transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 25.27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res; 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gench R;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: C90919

A;Residues: preliminary

A;Residues: 1-457 cHAY>

A;Residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ucuronide permease [imported] - Escherichia coli (strain 0157:H7, substrain RIMD 05099
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A.Cross-references: UNIPROT:P30868; UNIPARC:UPI0000137B23; GB:AE000257; GB:U00096; NID:g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Accession: B64918
R,Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cd
                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                142 IPVGFHLYSTHAALAALRGHFC--LSSDKMVCYLLKTKAIVNASEMDIQNV----PLSE 194
                                                                                                                                                                                                                     ----PFLVGIEGSLKGSTYNLL-FCGSCG 141
                                                                                                                                                                                                                                                                                       317 WSLPVALVALAIASIGOGVIMIVWWALEADIVEYGEYLIGVR--IEGLIYSLFSFTRKCG 374
                                                                                                                                                                                                                                                                                                                                                                                                               375 QAIG---GSIPAFILGLSGYIANQVQTPEVIMGIRTSIALVPCGFMLLAFVIIMFYPLTD 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Bscherichia coli
Bate: 18-7ul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
Accession: C90919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glucuronide permease uidB - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
                                                                                                                                                           Gaps
                                                                                                                                               53; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27;
                                                                             DB 2; Length 457;
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A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                 Query Match 6.8%; Score 81.5; DB Best Local Similarity 25.2%; Pred. No. 11; Matches 37; Conservative 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 KIABLKEKIVLTHNRLKSLMKILSEVT 221
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                                                                                                                                                                                                                     95 WDLSRSLGAVVFSRVTNNV-----VLEA
C; Superfamily: melibiose carrier protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: BCB2323
C,Superfamily: melibiose carrier protein
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Science 277, 1453-1462, 1997
A;Title: The complete genome seque
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Best Local Similarity
Matches 37; Conserval
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OM protein - protein search, using sw model

March 25, 2006, 07:56:15 ; Search time 231 Seconds
(without alignments)
699.420 Million cell updates/sec Run on:

US-09-942-052A-728 1198 1 MAAQPLRHRSRCATPPRGDF......LKSLMKILSEVTPDQSKPEN 229

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt 05.80:\*
1: uniprot sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	043482 homo sapien		Q4pab5 ustilago ma		Q9nyp9 homo sapien	homo	pan t	_	-	O9p802 schizosacch	Q4q626 leishmania	Q8sell oryza sativ	Q9ch87 lactococcus	Q69ke0 oryza sativ		Q50pd2 entamoeba h	Q50v43 entamoeba h	Q50wz8 entamoeba h	Q5m052 streptococc	Q96ep1 homo sapien	Q5m4r3 streptococc	Q65329 barley mild	-	Q75rz6 ciona intes	P14508 campylobact		Q6cx82 kluyveromyc	_	Q81013 mus musculu	Q97fq5 clostridium	Q5k2k3 isfahan vir
SUMMARIES	Ω	OIPS HUMAN	Q9CXR6 MOUSE	Q4PAB5 USTMA	Q9CZJ6 MOUSE	CU045 HUMAN	Q542Z0_HUMAN	CU045_PANTR	Q5BLB1_BRARE	OS4HI6_DICDI	YCZC_SCHPO	040626_LEIMA	Q8S611_ORYSA	Q9CH87_LACLA	Q69KE0_ORYSA	O83693_TREPA	Q50PD2_ENTHI	Q50V43_ENTHI	OSOWZ8_ENTHI	Q5M052_STRT1		Q5M4R3_STRT2	POL2 BAMMA	Q50XW7_ENTHI	Q75RZ6 CIOIN		Q68VH2 9POTY	Q6CX82 KLULA	Q4JTS4_CORJK	CHFR MOUSE	Q97FQS CLOAB	Q5K2K3_9RHAB
	DB	н	7	71	7	П	~	٦	7	0	Н	7	7	7	7	7	7	7		7	-	N	<del>,</del>	7	7	н	7	7	~	П	7	.73
	Length	229	218	462	204	233	233	232	207	532	155	1556	361	695	628	597	502	661	φ	633	9	735	893	152	638	250	493	634	969	9	699	2093
d	Query Match	100.0	10.2	9.8	9.6	9.4	9.4	9.5	9.1	8.9	8.8	7.8	7.7	7.7	7.6	7.6	7.5	7.5	7.5	7.4	7.4	7.4	7.4	7.4	7.4	7.3	7.3	7.3	7.3	7.3	7.2	7.2
	Score	1198	122	-	115.5	113	113	110.5	109	107			92	92	0	90.5	89.5	٠		89		83	83	88.5	•	88	8		87.5	87	86.5	86.5
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0529n3 magnaporthe 0839t4 enterococcu 04n664 arthrobacte 06gxe5 cochliobolu 068th4 barley mild 081hq7 nocardia un 081hu1 streptomyce 0815K5 plasmodium 06fkn6 candida gla 069k06 medicago sa 040360 medicago sa
0529N3 MAGGR 0939T4_ENTFA 0939T4_ENTFA 063NES_COCCA 0631Q7_9NOCA SYM1_STRAW 0815KS_PLAF7 06FXN6_CANGA GLSN MEDSA 040360 MEDSA 040360 MEDSA 040360 MEDSA 040360 MEDSA 040360 MEDSA 040360 MEDSA 040360 MEDSA 040360 MEDSA 040360 MEDSA
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  the Buropean Bioinformatics Institute. There are no restrictions on use as long as its content is in no way modified and this statement is
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MEDLINE=2108566; PubMed=11217851; DOI=10.1038/35055500;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Piukunishi Y., Komno H., Adachi J., Pukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saitor T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus.
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STRAIN=CS7BL/6J; TISSUE=Head;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Mus musculus 13 days embryo head CDNA, RIKEN [ull-length enriched library, clone:3110025H23 product:hypothetical protein, full insert
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                                                                                                                                                                                                                                                                                                                                                            Length 229;
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                                                                                                                                                                                                                                                          GO:0005515; F:protein binding; TAS.
GO:0007154; P:cell communication; NAS.
JENCE 229 AA; 24691 MW; 0EBD4006193A3106 CRC64;
                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1198; DB 1; I 100.0%; Pred. No. 8.8e-105;
                                                                                            EMBL; AF025441; AAC39561.1; ALT INIT; mRNA.
EMBL; BC015050; AAH15050.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                         IntAct; 043482; -.
Ensembl; ENSG0000104147; Homo sapiens.
HGNC; HGNC:20300; OIP5.
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01-JUN-2001 (TEBMBLrel. 17, Last seq
01-JUN-2001 (TEBMBLrel. 17, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                         Matches 229; Conservative
                                                                                                                                                                                              H-InvDB; HIX0012150; -. MIN; 606020; -. GO; GO:005515.
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                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the RIKEN Genome Exploration Research Group Phase I & II Team, "Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci P., Shibata Y., Hayateu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramateu M., Hayashizaki Y.; Shibata K., Itoh M., Wormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630 (2000).
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Adachi J., Alzawa K., Akahira S., Akimura T., Arai A., Anno H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Salto H., Saito R., Sakai K., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshino M.,
Muramatsu M., Hayashizaki Y.
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                            Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lions P., Marchionni L., Mashima J., Mazazerlli J., Mombaerte P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Saneshi H., Schoenbach C., Seya T., Shibate Y., Storch K.-P., Suzuki H., Toyo-oka K., Wang K.H., Wattz C., Whitteker C., Wilming L. Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Gariboldi M.,
Tee N.H.,
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamannoto R., Matsunnoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahikai M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Natsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKEN integrated sequence analysis (RISA) system-384-format genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                              Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CS7BL/6J; TISSUE-Head;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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Ensembl; ENSMUSG0000022978; Mus musculus.
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The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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RA ARTANS=521.

RA Ait--ahra M., Allen T., An P., Anderson B., Ant--ahra M., Allen N., Allen T., An P., Anderson B., Ant--ahra M., Allen N., Allen T., An P., Anderson M., Anderson S., Ant--ahra M., Allen N., Allen T., An P., Anderson M., Anderson S., Bary A. Blatchafflery B., Bloom T., Bloom T., Bly G., Barry A., Bayll T., Blitsheteyn B., Bloom T., Bly G., Borowsky M., Blatchafflery B., Callow G., Cooke J., Garain G., Garrie B., Blitch J., Harcher H., Rigdins H., Rigoptan D., Hagos B., Hall J., Harcher B., Heller A., Higgins H., R., Honan T., Horn A., Houde M., Hughes L., Hulme W., Hubby B., Iliev I., R., Lama D., Landers T., Levine S., Lewis D., Lewis T., Lucien O., Lewis D., Lewis D., Lewis T., Almblad-to-K., Liu X., Lokytleang T., Lokytleang T., Lucien O., R., Marabella R., Maru K., Matchews C., Maucell E., Manning J., Marbella R., Maru K., Matchews C., Maucell E., Manning J., Mannell E., Mannen G., Mayoen V., Malzain L., Minkoa T., Mikkelsen T., Mlenga V., Moru K., Norbu N., O'donnell P., Okoawo O., O'Leary S., Conctosho B., Retton R., Stalker A., Stanker S., Perrin D., Phunkhang P., Piqqani B., Retton R., Stalker J., Stanger D., Settipalli S., Sharpe T., Asamesany U., Sharpe T., Retton R., Stonker S., Perrin D., Vassiliev H., Topham K., Schupbach R., Seaman C., Settipalli S., Sharpe T., Ramala T., Tesma S., Yee S., 
                                 ----KTKAIVNASEMDIONVPLSEKIAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Fungi, Basidiomycota, Ustilaginomycetes,
Ustilaginomycetidae, Ustilaginales, Ustilaginaceae, Ustilago.
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nitted (FBB-2004) to the RMBL/GenBank/DDBJ databases.
CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry w
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                         199 LKEKIVLTHNRLKSLMKILSEVTPDQ 224
148 LYSTHAALAALRGHFCLSSDKMVCYLL-
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(TrEMBLrel. 31, 1
(TrEMBLrel. 31, 1
                                                                                                                                                                                                                                                                                                                                              Q4PABS USTMA PRELIMINARY;
Q4PABS;
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Hypothetical protein.
ORFNames=UM02948.1;
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SEQUENCE 462 AA; 4
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NUCLEOTIDE SEQUENCE
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OR PABS US
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49283 MW; EDDCFDF17757B509 CRC64;

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111 NNVVLEAPFLVGIE-GSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHPCLSSDKM 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 VCYLLKTKAIVNASEMDIQ------NUPLSEKIAELKEKIVLTH-NRLKS 212
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                                                                                                                                                                                                                                             AA-----GPQL--PSWLQPERCAVFQCAQCHAVLADSV-HLAWDLSRSLGAVVFSRVT
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Mus musculus 11 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2700078124 product:hypothetical protein, full
insert sequence (2610039C10Rik protein).
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                                                                 Gaps
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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                                                                 46;
   DB 2; Length 462;
                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CS7BL/6J; TISSUB=Whole body;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
9.8%; Score 118; DB 2; L 25.9%; Pred. No. 0.03; ive 28; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
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Q9CZJ6;
                                                          Conservative
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                                                          64;
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WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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STRAIN=C57BL/6; TISSUE=Eye;
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Last annotation update)
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16-OCT-2001 (Rel. 40, Last sequ
10-MAY-2005 (Rel. 47, Last anno
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STRAIN=C57BL/6; TISSUE=Bye;
Director MGC Project;
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nes 50; Conservative
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Homo sapiens (Human)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                     NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dowler S.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-2005
01-FEB-2005
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                                                                                                                                                                     Isogai T.;
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                                                                                                    WEDLINE=2138955; PubMed=12477932; DOI=10.1073/pnas.242603899;
WA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Atlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Atlastner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Batt N.K.,
Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Haieh R.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong D.,
A Batepleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Maramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
R.M. Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
R. Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.,Sun, Krzywinski M.I., Skalaka U., Smailus D.E.,
Butterfield Y.,Sun, Krzywinski M.I., Skalaka U., Smailus D.E.,
M. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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teimer C., Clancy K., Rynditch A., Gardiner K.; Criteria for genome organization: Criteria for gene identification and features of genome organization: nalysis of 6.5 Mb of DNA sequence from human chromosome 21.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 ASPITSMEWDIOVVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAVLADS
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(TrEMBLrel. 31, Last sequence update)
(TrEMBLrel. 31, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 AA.
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                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:1689;
-!- SIMILARITY: To S.pombe SpC970.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF231921; AAF72945.1; -; mRNA.
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Q542Z0;
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DVLKALQMKLWE 221
                                                247:215-232 (2000)
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                                 analysis of
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-LSWVASQEDTNCILLRCVSCNVSVDKEQXLSKREKENGCVLETLCCAGCSLNLGYVYR 153
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                                                                                                                                               "Signal Sequence and Keyword Trap in silico for Selection of Full-
Length Human cDNAs Encoding Secretion or Membrane Proteins from Oligo-
Capped cDNA Libraries.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification of pleckstrin-homology-domain-containing proteins with novel phosphoinositide-binding specificities."; Biochem. J. 351:19-31(2000).
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Pan troglodytes (Chimpenzee).

Bukaryote, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Ocsuki T., Ota T., Nishikawa T., Hayashi K., Suzuki Y., Yamamoto J., Wakamatsu A., Kimura K., Sakamoto K., Hatano N., Kawai Y., Ishii S., Saito K., Kojima S., Sugiyama T., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Nagai K., Sugano S.,
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Watanabe H., Fujiyama A., Hattori M., Taylor T.D., Toyoda A.,
Kuroki Y., Noguchi H., BenKahla A., Lehrach H., Sudbrak R., Kube M.,
                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21061410; PubMed=11001876; DOI=10.1042/0264-6021:3510019; Dowler S.J., Currie R.A., Campbell D.G., Deak M., Kular G., Downes C.P., Alessi D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification of FAPP1 interacting proteins.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK075281; BAC115.1; "; mRNA.
EMBL; AR397945; AR476498.1; -; mRNA.
SEQUENCE 233 AA; 25863 MW; A07522806C4B6221 CRC64;
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01-FEB-2005 (Rel. 46, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
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Hypothetical protein.
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MEDLINE-21388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschul M.J., Usdin T.B., Toshiyuki S., Carninci P., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Golffard G.G.,

Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 VHLAWDLSR-SLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLY 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTPKNLDYKRDLFCLSVEAIESYVLGSSEKQIV-SEDKELFNL---ESRVEIEKSLTQME 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASMWSSMSEDASV----ADMERARL--EEAAAA-----EERPLVFLCSGCRRPLGDS
Taenzer S., Galgoczy P., Platzer M., Scharfe M., Nordsiek G., Bloecker H., Hellmann I., Khatlevich P., Paabo S., Reinhardt R., Zheng H.-J., Zhang X.-T., Zhu G.-F., Wang B.-F., Fu G., Ren S.-X., Zhao G.-P., Chen Z., Lee Y.-S., Cheong J.-E., Choi S.-H., Wu K.-M., Liu T.-T., Haiao K.-J., Taai S.-F., Kim C.-G., Oota S., Kitano T., Kohara Y., Sairou N., Park H.-S., Wang S.-Y., Yaspo M.-L., Sakaki Y., "DNA sequence and comparative analysis of chimpanzee chromosome 22.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88; Indels
                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AL954205; CAH18576.1; -; Genomic DNA.
SEQUENCE 232 AA; 25832 MW; 6549B8BE369245E7 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.2%; Score 110.5; DB
27.1%; Pred. No. 0.065;
iive 29; Mismatches E
                                                                                                                                                                                            -!- SIMILARITY: To S.pombe SpC970.12.
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Name=LOC553502;
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QSBLB1;
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Bichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,

Bichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,

Sucgang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,

Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,

Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,

Pilcher K., Chen G., Saunders D., Sodergren B., Davis P.,

Rethornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,

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Ranborcher P., Desany B., Just E., Morio T., Rost R., Churcher C.,

Cooper J., Haydock S., Van Driessche N., Croin A., Goodhead I.,

Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,

Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,

Nardroper A., Felder M., Thangavelu M., Johnson D., Knights A.,

Loulseged H., Mungall K., Oliver K., Picie C., Quail M.A.,

Urushihara H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M.,

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Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;

"The genome of the social amoeba Dictyostellum discoldeum";

Nature 0:0-0 (2005).
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Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 AVFQCAQCHAVLADSVHLAWDLS-RSLGAVVFSRVTNNVVL-EAPFLVGIEGSLKGSTYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 AVFMCGKCKLPIGDS -- LSWAGSDDENNQIMLKRITDNIVVGKEPFVSGTRKELGCLVVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 LLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIVNASEMDIQNVPLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.1%; Score 109; DB 2; Length 20
25.5%; Pred. No. 0.077;
tive 28; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                    Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases EMBL; BC090521; AAH90521.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 AA; 22941 MW; AF1A0ACCF375A28C CRC64;
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Bukaryota, Mycetozoa, Dictyosteliida, Dictyostelium
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Last annotation update)
                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                     STRAIN-Singapore local strain; TISSUE-Embryo; NIH MGC Project;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 LEYQDTVHQQMTEITSLAVIIGQRL 194
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InterPro; IPR009090; D_amino_pept_C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 25.51
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                                                                                                              and mouse cDNA sequences.
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NUCLEOTIDE SEQUENCE.
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Query Match
Best Local Similarity
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STRAIN=Friedlin;
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SEQUENCE 15
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RA MEDLINE=21848401; FubMed=11859360; DOI=10.1038/nature724;
RA SGOURCE C. Gailliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A., Saguros J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S., RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgson G.,
RA Holroyd S., Horneby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Mongall K.L., Murphy L.D., Niblett D., Odell C.,
A Oliver K., Volnes L., Jones M., Leather S., McDonald S., McLean J.,
A Oliver K., Volnes L., Jones M., Leather S., McDonald S., McLean J.,
A Natherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,
A Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
A Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
A Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
A Woodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B.,
A Godden J.R., Volckaert G., Aert R., Robben J., Grymonprez B.,
A Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,
A Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.,
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A Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forbburg S.L.,
A Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
A Hill genne sequence of Schizosaccharomyces pombe.";
                                                                                                  131
                                                                                                                                   261
                                                                                                                                                          132 ---YNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLL-KTKAJVNASEMDI 187
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                                                                                                                                                                                           262 DCIYSLFYCSYCHSPLGRKYNKTSQKFKILNNHFVVDIGSITYYSVGGNNNIIVEDKNEI 321
                                                                                           77 VFQCAQCHAVLADSVHLAMDLSRSLGAVVFSRVTNNVVLEAPFLVGIEGSLKGST----
                                                                                                                  European Bioinformatics Institute. There are no restrictions on as long as its content is in no way modified and this statement is
                                   Length 532;
                                                                                                                                                                                                                           188 ONVPLS------EKIABLKEKIVLTHNRLKSLMKILSEVTPD 223
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   BAF75AB8CD7C1D5C CRC64;
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Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                  75;
                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein C970.12 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                        (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 47, Last annotation update)
                    Score 107; DB
                    Query Match
Best Local Similarity 22.9%; Pred. No. v...
Matches 38; Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                                                             155 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          pombe (Fission yeast).
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GeneDB_Spombe; SPCC970.12; -.

    -!- SIMILARITY: To human C21orf45.

 60715 MW;
                                                                                                                                                                                                                                                                                                                                             STANDARD;
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71 QPERCAVFQCAQCHAVLADSVHLAWDLSRS--LGAVVFSRVTNNVVLEAPFLVGIEGSLK 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         833 GGGELMQTDAGFSIEVESPIAFLYDDDVHRASQDVGQKRAREEPDGVGGAGEEDAAAG-- 890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 FLVGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVC----YLL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----VWYHLYK------HFCLSADKASCVIGMWLL 971
                                                                                                                                                                                                                                                                                                                                                                                   19 QP---SVFQCKKCFQIVGDS--NAWVISHREYLSFTLSDAVENSVRVEDTFKRSDDGL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 GGTERAIDQASFTTSME-----WDTQVVKGS-----SPLGPAGLGAEEPAAGPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J., Smith D., Collins M., Fosker N., Harris D., Oliver K., O'Neil S., Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G., Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.

EMBL, CT005268; CAJ08424.1; -; Genomic_DNA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0031055; P:chromatin remodeling at centromere; IMP.
GO; GO:0031055; P:chromosome segregation; IMP.
GO; GO:0016575; P:histone deacetylation; IMP.
GO; GO:0031066; P:regulation of histone deacetylation at cent.
Complete proteome; Hypothetical protein.
SEQUENCE. 155 AA; 17874 MW; A7AEBD0F93760B0B CRC64;
                                                                                                                                                                                                                                                                                          61; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68;
                                                                                                                                                                                                                                  Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ıl protein.
1556 AA; 170195 MW; F6FF7CDDFE8DCAS9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                            8.8%; Score 105; DB 1; 30.1%; Pred. No. 0.13;
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24.3%; Pred. No. 27;
iive 22; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1556 AA.
                                                                                                                                                                                                                                                                                          18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 QVDL----EMREDII 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 NVPLSEKIAELKEKIV 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, Hypothetical protein
                                                                                                                                                                                                                                                                                          41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      942 VL-----TRY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q40626 LEIMA PRELIMINARY;
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OBS611 ORYSA PRELIMINARY;
O8S611;
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ID 08
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"The complete genome sequence of the lactic acid bacterium Lactococcus
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                     lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).
EMBL; AE006319; AAK04949.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 VGDL--LLVKENEKIPADGLILSEALVDES 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP005934; BAD36600.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IIGRFAMB; TIGR01494; ATPASE_P-Cype; 2.
PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                               Interpro; IPR006416; Arpase-IB-hvy.
Interpro; IPR001757; Arpase-IB-hvy.
Interpro; IPR005834; Dehal Tike hydro.
Interpro; IPR008250; B1-82-Arpase-reg.
Pfam; PF00122; B1-82-Arpase; 1.
Pfam; PF00702; Hydrolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGRFAMS; TIGR01511; ATPASE-IB1 Cu; 1.
TIGRFAMS; TIGR01525; ATPASE-IB hvy; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                   InterPro; IPR006403; ATPase-IB1_Cu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 25.3.,
38; Conservative 2
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Q69KEO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
SEQUENCE 695 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00119;
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                                                                           RESULT 14
Q69KE0 ORY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 APTPLPFRRAVRAKAAQDGSGGTSSASPAVAST-----DVVVVPGSREATPSG-PASDPV 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 AGPOLP----SW--LQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTNNVVL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 AGRGSPAAVLSWEELOVEMGRLLEAGA--RVIGREIAEARGLEHRM----SELGNN--- 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 EAPFLVGIEGSLKGSTYNLL--FCGSCGI------PVGFHLYSTHAALAAL-----RGH 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 AARIGEEMSNRIYIGACHILACVRLAH-PELDLREILDQGEASDARKDVMEEVGDLGKSV 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 ----LSEIRGSLR-VTYTGLHQLAGKCGIKSTIPANPDEFSLTSSLAELAAAMEEIPSKH 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 FCLSSDKM-----VCYLLKTKAIVNASEMDIONV------PLSEKIAELKEKI 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEEPA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                        Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzaes, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 ;
                                                                                                                                                                                                                                                                                                               The Rice Chromosome 10 Sequencing Consortium, "In-depth view of structure, activity, and evolution of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21235186; PubMed=11337471; DOI=10.1101/gr.GR-1697R; Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.;
                                                                                                                                                                                                                                                                                                                                                                                                                             Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q., Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. EMBL, AC099400, AAL01599.1; -; Genomic_DNA. EMBL, AE017047; AAP51763.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.7%; Score 92; DB 2; Length 361; 25.3%; Pred. No. 6.4; tive 28; Mismatches 92; Indels
                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
Wing R.A., Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo Saski C., Henry D., Oates R., Simmons J.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 AA; 38804 MW; F883BB3E8B8FFF45 CRC64;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      695 AA.
                                                        Putative gypsy-type retrotransposon protein.
ORFNames=OSJNBa0096B22.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                         Science 300:1566-1569(2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity 25.3 61; Conservative
                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                    NCBI_TaxID=39947;
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Matches 6
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161 HF------CLSSDKWVCYLLKTKAIVNASB--MDI--------QNVPLSE-K 195
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GO:0016021, C:integral to membrane; IEA.
GO:001622, C:integral to membrane; IEA.
GO:0016224, F:ATP binding; IEA.
GO:0003824, F:CATP binding; IEA.
GO:0004081, F:CATP binding; IEA.
GO:0004081, F:CATP binding; IEA.
GO:0016820; F:Pydrolase activity, acting on acid anhydrid. . ; IEA.
GO:0046873; F:metal ion binding; IEA.
GO:0046873; F:metal ion transporter activity; IEA.
GO:0038122; P:metalointing; IEA.
GO:0038001; P:metal ion transport; IEA.
GO:0015992; P:proton transport; IEA.
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Sukaryota, Virtálplantae, Streptophyta, Embryophyta; Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75981 MW; 1B4947C3C2A0FA0F CRC64;
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PROSITE; PS00216; SUGAR TRANSPORT 1; UNKNOWN 1.
SEQUENCE 628 AA; 68281 MW; 3230B108C6061027 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Myosin heavy chain-like.
Name=P0023BI0.17;
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25.3%; Pred. No. 15;
ive 28; Mismatches 5
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141 YRRKAPTPSPSRRVARAKAAQDGSGGTSSASPAVAST-----DVVVVPGSREAAPSGL-A 194
                                                                                                                                                                                                                                                                                                                                                                                            --FSRVTNNVVLEAPFLVGIEGSLKGSTYNLL--F 136
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MEDLINE=98332770; PubMed=9655876; DOI=10.1126/science.281.5375.375;
Praser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
Dodson R.J., Gwinn M.L., Hickey B.K., Clayton R.A., Ketchum K.A.,
Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D.,
Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M.,
Utterback T.R., McDonald L.A., Artiach P., Bowman C., Cotton M.D.,
Weidman J.F., Smith H.O., Venter J.C.;
                                                                                                                             ----DFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGA
                                                                                                                                                                                                                                                                                                   ----TSMEWDTQVVKGSSPLGPA
                                                                       96; Gaps
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Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema
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   ; Score 91; DB 2; Length 628;
; Pred. No. 16;
34; Mismatches 82; Indels
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Phosphoribosylglycinamide formyltransferase, putative.
Treponema palliam...
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EMBL; AE001243; AAC65662.1; -; Genomic_DNA
PIR; D71293; D71293.
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88.0%; Pred. No. 17;
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InterPro; IPR003135; ATP-Grasp.
InterPro; IPR011761; ATP-GRASP.
Pfam; PF02222; ATP-Grasp; 1.
PROSITE; PS50975; ATP_GRASP; 1.
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th 7.6%; Similarity 23.7%; 66; Conservative 3.
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083693;
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01-NOV-1998
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Scoring table:

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Sequence 6596, Application US/09134000C
Patent No. 6617156
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BATENCOCCUS PAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1990-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
NUMBER: OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 6596
                                                                                                                                                                                                       Sequence 11409, A
Sequence 3335, Ap
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TITLE OF INVENTION: PLAANT PROMOTER a-GLUCURONIDASE GENE
CONSTRUCT
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
PRILING DATE: 08-DEC-1989
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 119,102
          US-08-804-227C-8

US-08-804-128-2

US-09-270-71-43496

US-09-800-170-3

5262177-5

US-09-600-823-1

US-09-920-804-2

US-09-920-804-2

US-09-920-804-2

US-09-920-804-2

US-09-920-804-4

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US-09-920-804-4

US-09-920-804-4

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US-09-93-949-4

US-09-949-101-35-988-4

US-09-949-101-433-3335
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US-09-134-000C-6596
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237, App
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402.824 Million cell updates/sec
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     GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-248-137-3
US-09-252-991A-19049
US-09-557-682-1
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US-09-285-040-3
US-09-949-016-10829
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                   95 WDLSRSLGAVVFSRVTNNV-----VLEA-----PFLVGIEGSLKGSTYNLL-FCGSCG 141
                                                                                                                                                                                                                                                                                     142 IPVGFHLYSTHAALAALRGHFC--LSSDKWVCYLLKTKAIVNASEMDIQNV-----PLSE 194
                                                                                                                                                                                                                                                                                                            95 WDLSRSLGAVVFSRVTNNV-----VLEA-----PFLVGIEGSLKGSTYNLL-FCGSCG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316 WSLPVALVALAIASIGQGVTWTVWWALEADTVEYGEYLTGVR--IEGLTYSLFSFTRKCG 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 IPVGFHLYSTHAALAALRGHFC--LSSDKMVCYLLKTKAIVNASEMDIQNV-----PLSE 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                       26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jefferson, Richard A.
APPLICANT: Wilson, Katherine J.
APPLICANT: Weader, Michael
TITLE OF INVENTION: GLUCURONIDE REPRESSORS AND USES THEREOF
CORRESPONDENCE: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6; Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: JEFFERSON, RICHARD A.
TITLE OF INVENTION: HOST CELLS TRANSFORMED WITH THE E.COLI
GLUCORONIDS PERMEASE GENE
                                                                                                                                 DB 6; Length 457;
                                                                                                                                                                       54; Indels
                                                                                                                                                                     30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.8%; Score 81.5; DE 25.2%; Pred. No. 2.9; Live 30; Mismatches
                                                                                                                               Query Match
6.9%; Score 83; Di
Best Local Similarity 25.2%; Pred. No. 2;
Matches 37; Conservative 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      | : | : | : | | | 432 K--KFKETVVEIDNRKKVQQQLISDIT 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 KIAELKEKIVLTHNRLKSLMKILSEVT 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,546
FILING DATE: 15-0CT-1993
PRIOR APPLICATION NUMBER: 447,976
FILING DATE: 31-0CT-1989
APPLICATION NUMBER: 264,586
FILING DATE: 31-0CT-1988
APPLICATION NUMBER: 119,102
FILING DATE: 10-NOV-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08882704A Patent No. 5879906
PILING DATE: 10-NOV-1987
APPLICATION NUMBER: 264,586
FILING DATE: 31-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 25.2*
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5879906
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Patent No. 5432081
                                                                           LENGTH: 457
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US-08-882-704A-6
                                                       ,SEQ ID NO:7:
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142 IPVGFHLYSTHAALAALRGHFC--LSSDKWCYLLKTKAIVNASEMDIONV----PLSE 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: GLUCURONIDE REPRESSORS AND USES THEREOF NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 25-JUN-1997
CLASSIFICATION: 435
                 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.8%; Score 81.5; Di
Best Local Similarity 25.2%; Pred. No. 2.9;
Matches 37; Conservative 30; Mismatches
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FILING DATE: 11-Sep-1998
CLASSIFICATION: <UNKNOWD>
                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INPORMATION:
NAME: No. 5879906tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 190106.404
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 KIAELKEKIVLTHNRLKSLMKILSEVT 221
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Patent No. 6429292
GENERAL INFORMATION:
APPLICANT: Jefferson, Richard A.
Leader, Milson, Katherine J.
SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 457 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SS: single
linear
                                                                                              ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                          Washington
        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-882-704A-6
                                                                              COUNTRY:
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US-09-151-957-6
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Gaps

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                                                                                                                                                                                                                            36 SMEWDTQVVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAW 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 PQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTNNVV----LEAPF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 GFPNQALREIKALQEME-DNOYVVQLKAVFPHGGGFVLAFEFMLSDLAEVVRHAQRPLAQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----- NNIVHRDLKPANL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78; Indels 83; Gaps
                                                                                                                                                                                          25;
                                                                                                                                                 DB 1; Length 1711;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 325;
                                                                                                                                                                                        17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09018576
Patent No. 5968800
GENERAL INFORMATION:
APPLICANT: Gerhold, David L.
TITLE OF INVENTION: CYCLIN-DEPENDENT PROTEIN KINASE
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/018,576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 GGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLG
                                                                                                                                                                                        8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Pred. No. 3.8; 24; Mismatches
                                                                                                                                           Query Match
6.7%; Score 80.5;
Best Local Similarity 29.6%; Pred. No. 28
Matches 21; Conservative 8; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 78.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, RY60-30
                                                                                                                                                                                                                                                                  753 SMQAGSAVVNLAWPSGPLGQGA
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TELECOMMUNICATION INFORMATION:
                           : 1711 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       325 amino acids
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Best Local Similarity 23.28
Matches 56; Conservative
          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                  788 EQPLKLGOELF 798
                                                                                                                                                                                                                                                                                                            96 DLSRSLGAVVF 106
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                                                                                      protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                            TYPE: amino a TOPOLOGY: lin MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                       US-08-342-930-2
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US-09-018-576-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        375 QAIG---GSIPAPILGLSGYIANQVQTPEVIMGIRTSIALVPCGFMLLAFVIIWFYPLTD 431
                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: OSTEOBLAST-TESTICULAR PROTEIN TYROSINE TITLE OF INVENTION: PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                               FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6422922temburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 190106.404
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.8%; Score 81.5; E
Best Local Similarity 25.2%; Pred. No. 2.9;
Matches 37; Conservative 30; Mismatches
                   APPLICATION NUMBER: US 08/882,704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/342,930
FILING DATE: 21-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                    LENGTH: 457 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08342930 Patent No. 5821084
                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 20
FELECOMMUNIÇATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T: OLMSTED, ELIZABE:
T: MAURO, LAURA J.
T: DAVIS, ALAN R.
T: DIXON, JACK E.
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (415) 813-5600
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                                                                                                                                                                                                                                                                                                      COPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 706141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: CA
                                                                                                                                                                                                                                                                                                                                          US-09-151-957-6
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APPLICANT:
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168 -- KMVCYLLKTKAIVNASEM-DIONVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQ 224
                                                                                            ---LEEVLPDV 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 GPPNQALREIKALQEME-DNQYVVQLKAVFPHGGGFVLAFEFMLSDLAEVVRHAQRPLAQ 101
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                                                                                188 DIEQLCYVLRILGTPNPQVWPELTELPDYNKIS-FKEQVPMP---
                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: Gerhold, David L.

TITLE OF INVENTION: CYCLIN-DEPENDENT PROTEIN KINASE
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSE: Merck & Co., Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 DIEQLCYVLRILGTPNPQVWPELTELPDYNKIS-FKEQVPMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 URRENT APPLICATION DATA: APPLICATION NUMBER: US/09/018,576
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23.2%; Pred. No. 3.8;
ive 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                           Sequence 12, Application US/09018576
Patent No. 5968800
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102 AQVKSYLQMLLKGV---AFCHA--
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ATTORNEY/AGENT INPORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 1988
TELECOMMUNICATION INFORMATION:
TELECHONE: 732/594-3905
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amino acid
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Best Local Similarity 23.2%
Matches 56; Conservative
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linear
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COMPUTER READABLE FORM:
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64 POLPSWLOPERCAVFOCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTNNVV----LEAPF 119
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APPLICANT: Gerhold, David L.
TITLE OF INVENTION: CYCLIN-DEPENDENT PROTEIN KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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                                                                                                                                                                                                                                                                                                                               US/09/248,13
                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                       ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, RY60-30
                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/018,576
Sequence 3, Application US/09248137
Patent No. 6030788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                            Floppy disk
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                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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Matches 56; Conserv
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ZIP: 07065-0907
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RESULT 10

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DB 2;
     TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
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                                                                                                                                                                                                                                                                                                                                            ;; Score 78.5; DE;; Pred. No. 6.3;
24; Mismatches
                     FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
                                                                     PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR PILING DATE: 2000-66-15
PRIOR PRILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR APPLICATION NUMBER: 135619
NUMBER OF SEQ ID NOS: 273
SOFTWARE: Patentin version 3.0
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Best Local Similarity 23.2%
Matches 56; Conservative
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SEQ ID NO 19049
LENGTH: 190
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US-09-771-161A-237
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                                                                   APPLICANT: Gerhold, David L.
TITLE OF INVENTION: CYCLIN-DEPENDENT PROTEIN KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/248,137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.6%; Score 78.5; DB 2; Best Local Similarity 23.2%; Pred. No. 3.8; Matches 56; Conservative 24; Mismatches 78;
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                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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             Sequence 12, Application US/09248137
Patent No. 6030788
GENERAL INFORMATION:
                                                                                                                                            3: Merck & Co., Inc.
P.O. Box 2000, RY60-30
                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/018,576
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAMB: Hand, J. Mark
REGISTRATION NUMBER: 36,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 732/594-3905
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TOPOLOGY: linear
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                                                                                                                                                                                                                       COUNTRY: US
ZIP: 07065-0907
                                                                                                                                              ADDRESSEE: Mei
STREET: P.O. I
CITY: Rahway
STATE: NJ
                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
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US-09-248-137-12
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Sequence 19045, Application US/09252991A
Sequence 19045, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
ADPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PELING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
                                                           12;
                                                                                                                                                                                                                                                                            64 PQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTNNVV----LEAPF 119
                                                                                                                                                                          43 GPPNQALREIKALQEME-DNQYVVQLKAVPPHGGGFVLAFEFMLSDLAEVVRHAQRPLAQ 101
                                                                                                                                                                                                                                                                                                                                                                                                168 --KMVCYLLKTKAIVNASEM-DIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQ 224
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                                                           Gaps
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Length 452;
                                                     78; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 LPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTN-----NVVLEAPF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 LLPIYEDEGATTFNMF----SVKVAMDLYDKLANVTGTKYENYTLTPEEVLEREPF 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 LK--KEGLKGA-----GVYLDFRNNDARLVIDNIKKAAEDGAYLVSKMKAVGFLY 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 DFCGGTERAIDQASFTTSM-----EWDTQVVKGSSPLGP----AGLGAEEPAAGPQ 65
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6.4%; Score 77; DB 2; Length 607;
Best Local Similarity 23.2%; Pred. No. 15;
Matches 49; Conservative 30; Mismatches 76; Indels
                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: TAKEUCHI, Kenichi
APPLICANT: KOIDE, YOSHINAO
APPLICANT: NAKAHUSHI, Yuji
APPLICANT: NAKAHUSHI, Yuji
APPLICANT: SUZUKI, Satoru
TITLE OF INVENTION: L-ALPHA-GLYCEROPHOSPHATE OXIDASE GENE, ITILE OF INVENTION: L-ALPHA-GLYCEROPHOSPHATE OXIDASE GENE FILE REFERENCE: AZO-121814C/KI
CURRENT APPLICATION NUMBER: US/09/537,682
CURRENT PILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Enterococcus faecium No. 6303357 7044
US-09-537-682-1
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APPLICANT: Kennard, Malcolm
TTTLE OF INVENTION: Use of p97 and I
TITLE OF INVENTION: as Diagnostic ar
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bereskin & Parr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jefferies, Wilfred A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: McGeer, Patrick L.
APPLICANT: Rothenberger, Sylvia
APPLICANT: Food, Michael R.
                                                                                                                                                Sequence 1, Application US/09537682
Patent No. 6303357
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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40 King Street West
                                         140 PAPPRWPRRRCA 152
64 PQLPSWLQPERCA 76
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SEQ ID NO 1
LENGTH: 607
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GENERAL INFORMATION:
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US-08-520-933-3
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221 TLPSWGQALLSQDFELLCRDGSRADVTEWRQCHLARVPAHAVVVRADTD---GGLIF-RL 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 TNNVVLEAPFLVGIEGS----LKGSTY---NLLFCGSCG--IPVGFHLYST---HAALAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 LRGHFCLSSDKMVCYL----LKTKAIVNASEMDIQNVPLSEKIAELKEKIVLTHNRLKSL 213
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6.4%; Score 77; DB 1; Length 719;
Best Local Similarity 23.7%; Pred. No. 19;
Matches 59; Conservative 25; Mismatches 87; Indels
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APPLICANT: Jefferies, Wilfred A.
APPLICANT: McGer, Patrick L.
APPLICANT: Rothenberger, Sylvia
APPLICANT: Food, Michael R.
APPLICANT: Tood, Michael R.
APPLICANT: Yamada, Tatsuo
APPLICANT: Yamada, Tatsuo
APPLICANT: Yamada, Malcolm
TITLE OF INVENTION: Use of p97 and Iron Binding Proteins
TITLE OF INVENTION: as Diagnostic and Therapeutic Agents
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 RGDSSG--EGVCDKSPLERYYDYSGAFRCLAEGAGDVAFVKHSTVL-
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FAPLICATION NUMBER: US/08/520,933
FILING DATE: August 31, 1995
CLASSIFICATION: 424
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                               38,798
- 7685-006
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                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Shoma S. McDiarmid
REGISTRATION NUMBER: 38,798
REFERENCE/DOCKET NUMBER: 7685
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-364-7311
TELEPHONE: 416-361-1398
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40 King Street West
                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 719 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-520-933-3
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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333 MKGLLC-DPNRLPPYLRWCVLSTPEIQKCGDM------AVAFRRQRLKPE 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- ERCAVFOCAQCH--AVLADSVHLAWDLSRSLGAVVFSRV 109
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Best Local Similarity 23.7%; Pred. No. 19;
Matches 59; Conservative 25; Mismatches
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/285,040
FILING DATE: 01-APR-1999
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GEAVALIE, Micheline
REGISTRATION NUMBER: 40,261
TELECOMOUNICATION INFORMATION:
TELEFRONE 416-364-731
TELEFRONE: 416-361-1398
TELEFRONE: 416-361-1398
TELEFRONE: 416-361-1398
TELEFRONE: 416-361-1398
TELEFRONE: 416-361-1398
TOPOLOGY: 11near
NOLECULE TYPE: procein
US-09-285-040-3
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Search completed: March 25, 2006, 08:04:49
Job time : 48 secs

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                                                                            March 25, 2006, 08:14:45; Search time 165 Seconds (without alignments) 579.896 Million cell updates/sec
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1198
1 MAAQPLRHRSRCATPPRGDF......LKSLMKILSEVTPDQSKPEN 229
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Sequence
Sequence
Sequence
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| cgn2 6/ptodata/1/pubpaa/USO7 PUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO8-PUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO9-PUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO9-PUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO108-pUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO108-pUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO108-pUBCOMB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-09-942-052-730
US-09-942-052-704
US-09-942-052-704
US-09-80-688-82
US-10-408-765A-969
US-10-437-967-154548
US-10-369-493-18389
US-10-369-493-18389
US-10-437-967-186569
US-10-437-967-186569
US-10-437-967-186569
US-10-437-967-186569
US-10-188-125A-51802
US-10-188-125A-51802
US-10-16-761-10954
US-10-16-761-10954
US-10-16-761-10954
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US-10-437-963-147897
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                                                                                                                                                                                                                                   1867569 segs, 417829326 residues
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                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match
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                                                                                                                                                                  Sequence:
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Perfect
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sequence 66220, A Sequence 11748, A Sequence 115342, Sequence 115342, Sequence 281194, Sequence 51058, A Sequence 59, Appl Sequence 598, Appl Sequence 568, Appl Sequence 57058, A Sequence 67058, A Sequence 6705		A ENTITLED 85PJ CANCER 3/OIP5 5.229; 0; Gaps	գգ ,	VFSRVTNNVVLEAPFL 120                    VFSRVTNNVVLEAPFL 120
US-10-425-114-66220 US-10-195-518-6 US-10-450-763-31748 US-10-631-467-1618 US-10-631-467-1618 US-10-425-115-281194 US-10-425-115-281194 US-10-425-763-51058 US-10-029-345A-38 US-10-059-345A-38 US-10-057-135-59 US-10-957-135-59 US-10-957-135-59 US-10-957-135-59 US-10-957-135-59 US-10-957-135-59 US-10-424-599-968 US-09-925-299-968 US-09-925-299-968 US-09-925-299-968 US-10-450-763-44919	ALIGNMENTS	ULT 1  09-942-052-728  ublication No. US20030170626A1  ublication No. US20030170626A1  ENERAL INPORMATION:  APPLICANT: Raitano, Arthur B.  APPLICANT: Raitano, Arthur B.  APPLICANT: Raitano, Arthur B.  APPLICANT: Heart, Rane S.  APPLICANT: Ge, Wanny  APPLICANT: Ge, Wanniel  CURRENT APPLICATION NUMBER: US/09/942,052  BRIOR APPLICATION NUMBER: 60/228,432  RUMBER OF SEQ ID NOS: 744  SOFTWARE: PAT  SOFTWARE: PAT  ON 728  ELENGTH: 229  TYPE: RPT  CORGANISM: Unknown Organism  FEATURE: RPT  CORGANISM: Unknown Organism  FEATURE: RPT  COTHER INFORMATION: clone A protein  OTHER INFORMATION: clone A protein	MAAQPLRHKSRCATPPRODFCGGTERAIDQASFTTSMEWDTQVKGSSPLGFAGLGAEE. 	AAGPQLPSWIQPERCAVFQCAQCHAVLADSVHLAWDLSRSIGAVVFSRVTRNNVYLEAPFL 
278 457 457 1960 1960 2850 2850 46 2850 46 3005 544 46 44 44 44 44 44 44 44 44 44 44 44 4		tthur B.  tthur B.  tthur B.  nne S.  nne S.  id, Pia M.  CCLEIC ACID  SEFUL IN TY  20028 00  MBER: US/0  MBER: US/0  2008 28  744  100.08;  100.08;  tive O;	CATPPRGE	PERCAVEC 
		SULT 1  -09-942-052-728  Sequence 728, Application US/09942052 Sequence 728, Application US/09942052 Sequence 728, Application US/09942052 Sequence 728, Application US/09942052 SEPLICANT: Raitano, Arthur B. APPLICANT: Raris, Mary APPLICANT: Hubert, Rane S. APPLICANT: Ge, Wangmao, TITLE OF INVENTION: NUCLEIC ACID AND TITLE OF INVENTION: NUCLEIC ACID AND FILE REFERENCE: 51158-20028.00 CURRENT APPLICATION NUMBER: US/09/942 CURRENT APPLICATION NUMBER: G6/228,432 PRIOR FILING DATE: 2000-08-28 RIOR FILING DATE: 2000-08-28 SOU ID NO 728 LENGTH: 229 TYPE: PAT ORGANISM: Unknown Organism PERTURE: OTHER INFORMATION: Clone A protein OTHER LOCAL Similarity 100.0%; Score Best Local Similarity 100.0%; Pred.	AAQPLKHKSK 	AGPQLPSWLO           AGPQLPSWLO
81.5 81.5 81.5 81.5 81.5 80.5 80.5 80.5 80.5 79.5 79.5	•	ULT 1 09-942-052-728 dequence 728, Applic ublication No. US20 ENERAL INFORMATION: Fariano, APPLICANT: Raitano, APPLICANT: Raitano, APPLICANT: Afar, D APPLICANT: DAIL ITILE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION FILE REFERENCE: 511 TITLE OF INVENTION FILE REFERENCE: 51 TITLE OF INVENTION FORWART APPLICATION ONGANISM: DAFE TYPE: PRT ONGANISM: UNKNOWN FEATURE: OGRANISM: OGNES  OGRANISM: OGNES OG		61 A 61 A
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VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIV 180 

61 121

g ò d NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN 229

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Sequence

US-10-213-974+36 US-10-424-599-226730 US-10-369-493-9793

Sequence

Sequence Sequence Sequence

-10-425-115-216789 -10-425-114-42310

181 NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN

229

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                                                                                                                  APPLICANT: Feater, Reaf,
APPLICANT: Hubert, Rene S.
APPLICANT: Afar, Daniel
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
TITLE OF INVENTION: USEPUL IN TREATMENT AND DETECTION OF CANCER
FILE REPERENCE: 51158-2000-028.00
CURRENT APPLICATION NUMBER: U5/09/942,052
CURRENT PILING DATE: 2001-08-28
PRIOR PPLICATION NUMBER: 60/228,432
PRIOR FILING DATE: 2000-08-28
NUMBER OF SEQ ID NOS: 744
SOFTWARE: PATENTING OF SEQ ID NOS: 744
SOFTWARE: PATENTING OF SEQ ID NOS: 2.1
SEQ ID NO 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFL 120
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APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Hubert, Rene S.
APPLICANT: Afar, Daniel
APPLICANT: Afar, Daniel
APPLICANT: Challita-Eid, Pia M.
TITLE OF INVENTION: WUSEFUL AND CORRESPONDING PROTEIN ENTITLED 85P1B3
TITLE OF INVENTION: WUSEFUL N. TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20028.00
CURRENT APPLICATION NUMBER: US/09/942,052
CURRENT FILING DATE: 2001-08-28
PRIOR PELLOATION NUMBER: 60/228,432
PRIOR FILING DATE: 2000-08-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Unknown Organism: 85P1B3/OIP5; OTHER INFORMATION: protein sequence
US-09-942-052-729
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Sequence 729, Application US/09942052
Publication No. US20030170626A1
GENERAL INFORMATION:
APPLICANT: Raitano, Arthur B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Unknown Organism
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 730
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61 AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPPL 120
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APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Ge, Wangmao
APPLICANT: Challita-Eid, Pia M.
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20028.00
CURRENT APPLICATION NUMBER: US/09/942,052
CURRENT PILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 60/228,432
PRIOR FILING DATE: 2000-08-28
NUMBER OF SEQ ID NOS: 744
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 331
ORGANISM: Unknown Organism
PEATURE:
OTHER INFORMATION: Description of Unknown Organism: 85PlB3 protein
OTHER INFORMATION: sequence
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                                                                                                                                                                    Length 229;
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                                                                                                                                                                 Query Match
100.0%; Score 1198; DB 3;
Best Local Similarity 100.0%; Pred. No. 9.8e-114;
Matches 229; Conservative 0; Mismatches 0;
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Publication No. US20030170626A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 229; Conservative
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US-09-942-052-731
                                                                                     , OTHER INFORMATUS-09-942-052-730
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APPLICANT: Faris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Ge, Wangmac
APPLICANT: Ge, Wangmac
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
TITLE OF INVENTION: USEFUL N TREATMENT AND DETECTION OF CANCER
FILE REPERENCE: 51158-20028.00
CURRENT APPLICATION NUMBER: US/09/942,052
PRIOR APPLICATION NUMBER: 2001-08-28
PRIOR PILING DATE: 2000-08-28
PRIOR PILING DATE: 2000-08-28
NUMBER OF SEQ ID NOS: 744
SOFTWARE PATENTION OF 2.1
SEQ ID NO 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Unknown Organism: Splice variant 1 OTHER INFORMATION: open reading frame 3 peptide sequence
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NAME/KEY: MOD RES
LOCATION: (50)..(51)
OTHER INFORMATION: Unknown amino acid or stop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MOD RES
LOCATION: (67)
OTHER INFORMATION: Unknown amino acid or stop
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; OTHER INFORMATION: Unknown amino acid or stop
US-09-942-052-707
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                                                 Sequence 707, Application US/09942052
Publication No. US20030170626A1
GENERAL INFORMATION:
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Publication No. US20030170626A1
GENERAL INFORMATION:
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Hubert, Rene S.
Afar, Daniel
Ge, Wangmao
Challita-Eid, Pia M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Unknown Organism
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LOCATION: (44)
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RESULT 5
US-09-942-052-707
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US-09-942-052-704
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED BSP1B3
TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REPERRNCE: 51158-20028 00
CURRENT APPLICATION NUMBER: US/09/942,052
CURRENT FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 60/228,432
PRIOR APPLICATION NUMBER: 60/228,432
PRIOR APPLICATION NUMBER: 60/228,432

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

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96 --LSWVASQEDTNCILLRCVSCNVSVDKEQKLSKREKENGCVLETLCCAGCSLNLGYVYR 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 VHLAWDLSR-SLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLY 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 STHAALAALAALKGHFCLSSDKMVCYLL--KTKAIVNASEMDIONVPLSEKIAELKEKIVUTH 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 ASMWSSMSEDASV----ADMERAQL--EEEAAAAE-----ERPLVFLCSGCRRPLGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 ASFITSMEWDTQVVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAVLADS
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                 FEATURE:
OTHER INFORMATION: Description of Unknown Organism: 85P1B3 peptide
COTHER INFORMATION: sequence
US-09-942-052-704
                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.4%; Score 113; DB 3; Length 233; Best Local Similarity 27.1%; Pred. No. 0.0075; Matches 52; Conservative 30; Mismatches 88; Indels 22;
                                                                                                                                                                                                                                                                                                  11.5%; Score 138; DB 3; Length 29; 100.0%; Pred. No. 1.2e-06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Scient KATO
APPLICANT: Chikashi KGUCHI
APPLICANT: Chikashi EGUCHI
APPLICANT: Chikashi EGUCHI
APPLICANT: Mihoro SAEKI
TITLE COF INVENTION: Human Proteins and CDNAs thereof
FILE REFERENCE: 2001-1102A/WMC/00653
CURRENT APPLICATION NUMBER: US/09/890,688
CURRENT FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US/09/890
PRIOR APPLICATION NUMBER: US/000-31062
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 2000-02-08
PRIOR FILING DATE: 2000-02-09
PRIOR PRILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: US/2000-34090
PRIOR PRILING DATE: 2000-02-10
PRIOR PRILING DATE: 2000-02-14
PRIOR PRILING DATE: 2000-03-14
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 160
                                                                                                                                                                                                                                                                                                                                                                                                                172 YLLKTKAIVNASEMDIQNVPLSEKIAELK 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YLLKTKAIVNASEMDIQNVPLSEKIAELK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 82, Application US/09890688
Publication No. US20030144475A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 29; Conservative
NUMBER OF SEQ ID NOS: 744
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 704
LENGTH: 29
                                                                                                             TYPE: PRT
ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
US-09-890-688-82
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LENGTH: 233
TYPE: PRT
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Jardauk, Brad

TITLE OF INVENTION: Brad Molecules and Other Molecules Associated With; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement; FILE REPERBRICE: 38-21(5321)B

CURRENT APPLICATION WUMBER: uS/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 154548

Libright: 361

TYPE: """
                                                                                                                                                                                                                                                                                225 LINHRIKAATIPSASDASPPPPRRQSIVTIGEKBARAKAARAKSGGTSSA----SPTTVST 279
                                                                                                                                                                                                                                                                                                                                                             280 DVVPVVGSQEVTPSG-PISDPAGGPSLPEAVLTWEELQVEMGRLLKAGARGIGREISEAR 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                              85 AVLADSVHLAWDLSRSLG-----AVVFSRVTNNVVLE-----APFLVGIEGSLK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339 AETAAANALAERLVRELAEAREDLTKMRELVAGNERQSKGLEDRMSELGDNLSEIRGSLR 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 GSTYNLL--FCGSCG----IPVG---FHLYSTHAALAALRG-----HFCLSSDKM----- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                399 -VTYTGLHQLAKECGVKSTIPVNLDBFSLTSSLAELATAMGEIPSKHTSRIAEETSNGIY 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 AGRGSPAAVLSWEELOVEMGRLLEAGA--RVIGREIAEARGLEHRM----SELGNN--- 152
                                                                                                                                                                                                                                                                                                                                  40 DTQVVKGSSPLGPAGLGAEEPAAGPQLP----SW--LQPERCAVF-----QCAQCH
                                                                                                                                                                                                                                     -----CGTERAIDQASFITSMEW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 --VCYLLKTKAIVNAS--EMDIQNV-------PLSEKIAELKEKIV 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      458 TGVCHVL---ACVRLSRPELDLREILDQGAASDTRKEVMEEVSDLGESVL 504
                                                                                                                                                                                        101;
                                                                                                                                      Length 708;
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                                                                                                                                                                                      Indels
                                                                OTHER INFORMATION: Clone ID: PAT_MRT4530_91377C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Clone ID: PAT_MRT4530_54398C.1.pep
US-10-437-963-154548
                                                                                                                                                                                        96;
                                                                                                                                           DB 4;
                                                                                                                                      8.0%; Score 95.5; DB
24.5%; Pred. No. 2.1;
:ive 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 154548, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Brabazuk, Brad
                                                                                                                                                                                                                                     6 LRHRSRCATPPRGDF-----
                                                                                                                                    Query Match
Best Local Similarity 24.5'
Matches 71; Conservative
TYPE: PRT ORGANISM: Oryza sativa FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Oryza sativa
                                                                        ; ОТНЕК 110-437-195427
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 ASFITSMEWDTQVVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAVLADS
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                                                                                                                                                                                                                                                                                                 APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Gibson, Bradford W.
APPLICANT: Gibson, Bradford W.
APPLICANT: Glann, Gary M.
APPLICANT: Marnock, Dale B.
TITLE OF INVENTION: TARGERS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROFEOME
FILE REFERENCE: 660098.465
CURRENT APPLICANTION NUMBER: US/10/408,765A
CURRENT PILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 113; DB 4; Length 233;
; Pred. No. 0.0075;
30; Mismatches 88; Indels
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                                                                                                                                                                                 Application US/10408765A
5. US20040101874A1
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Barbazuk, Brad
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APPLICANT: Kovalic, David K.
APPLICANT: Chou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                         APPLICANT: Ghosh, Soumitra S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 27.19
Matches 52; Conservative
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210 DVLKALQMKLWB 221
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210 DVLKALQMKLWE 221
                 208 NRLKSLMKILSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-969
                                                                                                                                                                              Sequence 969, Applic
Publication No. US20
GENERAL INFORMATION:
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LENGTH: 708
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LENGTH: 233
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APPLICANT:
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Query Match
Best Local Similarity 23.0%;
Matches 52; Conservative 26
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Oryza sativa FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-10-437-963-155606
US-09-780-525-2
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Publication No. US20030233675A1

GRNERAL INFORMATION:

APPLICANT: Stater, Steven C.

APPLICANT: Stater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Green C.

APPLICANT: Goldman, Barry S.

APPLICANT: Green C.

APPLICANT: Green C.

APPLICANT: Goldman, Barry S.

APPLICANT: Green C.

APPLICANT: Gree
                                                                 101 LGAVVPSRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 HP------CLSSDKWVCYLLKTKAIVNASE--MDI------ONVPLSE-K 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 92; DB 4; Length 695;
; Pred. No. 4.7;
28; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Xiactong Li
TITLE OF INVENTION: FHARL, A NEW RING FINGER PROTEIN
FILE REFERENCE: GP-70668-C1
CURRENT APPLICATION NUMBER: US/09/780,525
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 09/456,876
PRIOR PILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 2
SOFFWARE: PASKSEQ for Windows Version 3.0
                    ----VCYLLKTKAIVNASEMDIQNV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 IAELKEKIVLTHNRLKSLMKILSEVTPDQS 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 VGDL--LLVXENEKIPADGLILSEALVDES 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09780525
Patent No. US20020004223A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Lactococcus lactis US-10-369-493-18389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Priya Chaturvedi
Mark R. Hurle
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ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 38; Conserva
                    162 FCLSSDKM
                                                                                                                                                                                                              267 L 267
                                                                                                                                                204 V 204
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NOS: 204966
                                                                                                                                                                        491 PMPDRRABREQDPRVAPQ------QCAVC---LQPPCHLYWGCTRTGCYGCLA 534
                                                                                                                                                                                                                                                                                                                                                                                              100 ----SLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTY-NLLFCGSCGIPVGFHLYSTHA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 EDPSPQPGVPLILLP-----LCCRCYAKEICSEYVVRTTDLVNHI------LNSNAIS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 EEPAAGPQLPSWLQPERCAVFQCAQCHA--VLADSVHLAWDLSRSLGAVVFSRVTNNVVL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 EAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALAGHFCLSSDKMVCYLLK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 EGPF-----CATTDSKKY-LGSAS---AFSVKQTEWP------CATTDSKKY-LQ 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 AAQPL--RH--RSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 APEPLSCRHGRHLRCAAVD-----GAGRETERPSPPAPQ-----REESPSGSLGAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59; Gaps
                                                                                                                               8 HRSRCATPPRGDFC-----GGTERAIDQA----SFTTSMEWDTQVVKGSSPL
                                                                    74;
                                                                                                                                                                                                                                                              51 ---GPAGLGAEEPAAGPOLPSWLOPERCAVFOCAQCHAVLADSVHLAWDLSR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 ALAALRGHFCLS----SDKMVCYLLKTKAIVNASEMDIQNVPLSE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Clone ID: PAT_MRT4530_83357C.1.pep
US-10-437-963-186569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 TKAIVNASEMDIQN-----VPLSEKIAELKEKIVLTH 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 NGSFGGITEDEEQSSLXNFLYPSKELLPDDKEMSIFDH 211
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7.4%; Score 88.5; DB 4;
Best Local Similarity 22.9%; Pred. No. 5.6;
Matches 50; Conservative 27; Mismatches 82;
; Score 89; DB 3; Pred. No. 8.9; 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 186569, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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Boukharov, Andrey A.
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----FC--ENTLSCKPQMVKSIVHFASREAMNIEGFSEKTAEQLFEK-- 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96 DLSR----SLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNL-----LFCGSCGIPVGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 31; Gaps
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7.2%; Score 86.5; DB
Best Local Similarity 27.4%; Pred. No. 16;
Matches 37; Conservative 22; Mismatches
                                                                                       PRIOR APPLICATION NUMBER.

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/200,335

PRIOR PILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06
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Job time : 166 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                           RIOR FILING DATE: 2000-12-22
RIOR APPLICATION NUMBER: 60/267,636
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                  RIOR APPLICATION NUMBER: 60/257,931
RIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
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                                                                                                                                                                                                                                                                    2000-09-09
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Remaining Prior App
NUMBER'OF SEQ ID NO
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                                                                                                                                                                                                                                                                    Molecules Associated With
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 YVSCGSVIEMSROMKAARAGVRAQSXPACXGIPTVGKVGSV--LLFTARMGEGLCHMFTT 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 TLGPDVPEGARPRGRLCLPQASGHDTPGPISPTSLVLNKRTRIEIDEVVATMDISEANEG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 GSKAMECGVKMCLVGWPWLAWDELGPRSGYQFGLNHRRPLVKAVLDGHLCEEEDAVNCLP 322
                                                                                                                               ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules As; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement; CURRENT APPLICATION NUMBER: US/10/437,963; CURRENT FILING DATE: 2003-05-14; NUMBER OF SEQ ID NOS: 204966; SEQ ID NO 155606; LENGTH: 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: AV, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323 KLRKTVGSASE-----AKEAVKPAVKOEKKIRS-VKVLSLVS-DLSLP 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AAGPQLPSWLQPERCAVFQCAQCH-------AVLADSVHLAWDLSR--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 87.5; DB 4; Length 84; Pred. No. 18; 23; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 PRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_55353C.1.pep
US-10-437-963-155606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)..(848)
OTHER INFORMATION: unsure at all Xaa locations
Sequence 155606, Application US/10437963
Publication No. US20040123343A1
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Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.3%;
                                                                 La Rosa, Thomas J.
Kovalic, David K.
Zhou, Yihua
Cao, Yongwei
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Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
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Best Local Similarity 22.1:
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wall, Daniel
Trawick, John
Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT
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GenCore version 5.1.7
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March 25, 2006, 08:15:45; Search time 24 Seconds (without alignments) 281.425 Million cell updates/sec
  - protein search, using sw model
OM protein
                                       Run on:
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US-09-942-052A-728 1198 score: Title: Perfect sc Sequence:

1 MAAQPIRHRSRCATPPRGDF..........LKSLMKILSEVTPDQSKPEN 229

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

174695 segs, 29494374 residues Searched:

Total number of hits satisfying chosen parameters:

174695

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/SIDSS/pcdata/1/pubpaa/US08 NEW PUB.pep:\*
/SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pep:\*
/SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pep:\*
/SIDSS/ptodata/1/pubpaa/PCT NEW PUB.pep:\*
/SIDSS/ptodata/1/pubpaa/US09 NEW PUB.pep:\*
/SIDSS/ptodata/1/pubpaa/US010 NEW PUB.pep:\*
/SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pep:\*
/SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pep:\*
/SIDSS/ptodata/1/pubpaa/US060\_NEW\_PUB.pep:\* Published Applications AA New:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		de.				
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
	98	7.2	584	-	US-11-096-568A-12723	Semience 12723. A
2	86	7.2	619	1	TIS-11-096-568A-12722	Company 12722
ım	86	7.2	644	. [	US-11-096-568A-12721	Segmence 12721, A
4	80.5	6.7	1711	7	US-11-143-984A-38	
s	79.5	9.9	227	7	US-11-096-568A-19014	1901
9	79.5	9.9	278	7		
7	79.5	9.9	282	7	US-11-096-568A-19012	Н
8	79.5	9.9	306	7	US-11-172-740-327	(7)
60	79	9.9	482	7	US-11-229-371-87	87.
10	. 79	9.9	482	7	US-11-229-371-177	177.
11	79	9.9	482	7	US-11-228-923-87	87.
12	79	9.9	482	7	US-11-228-923-177	177.
13	79	9.9	482	7	US-11-228-875-87	87, A
14	79	9.9	482	7	US-11-228-875-177	177.
15	79	9.9	1705	7	US-11-143-984A-37	37, 4
16	77.5	6.5	462	7	US-11-087-099-12028	120
17	76.5	6.4	400	7	US-11-229-371-2	~
18	76.5	6.4	400	7	US-11-228-923-2	~
19	76.5	6.4	400	7	US-11-228-875-2	7
20	16	6.3	1001	7	US-11-072-512-2283	228
21	75.5	6.3	8695	7	US-11-205-109-15	15, A
22	75	6.3	295	-	US-11-172-740-323	323.
23	75	6.3	458	7	US-11-069-642-3	3, At
24	74.5	6.2	267	7	US-11-087-099-9317	93
25	74.5	6.2	467	7	US-11-096-568A-11427	

Sequence 4, Appli Sequence 9, Appli Sequence 219, App	Sequence 2, Appli Sequence 73, Appl		Sequence 48, Appl Sequence 30876, A	Sequence 30875, A			Sequence 24484, A Sequence 24483, A		Sequence 752, App.	Sequence 90, Appl	Sequence 3468, Ap	Sequence 758, App
US-11-075-185-4 US-11-140-625-9 US-10-644-807-219	US-11-127-622-2 US-11-127-877-73	US-11-087-099-7267 US-11-186-284-26	US-11-143-980-48 US-11-096-568A-30876	US-11-096-568A-30875 US-11-096-568A-30874	US-11-087-099-12205	US-11-096-568A-24485	US-11-096-568A-24484 US-11-096-568A-24483	US-11-072-512-3758	US-11-055-822-752	US-11-203-251A-90	US-11-072-512-3468	US-10-330-773-758
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3689 323 428	428	3063	7102	327	378	532	638 644	205	388	1006	229	273
9 9 9	6.2	999	6.1	6.1	6.1		6.1	6.0	6.0	0.9	5.9	5.9
74.5	74	4 4 .	73	73	72.5	72.5	72.5	72	72	71.5	7.1	71
26 27 28	30	32.	34	32 36	37	38	2, 4, 2, 0	41	42	43	44	45

# ALIGNMENTS

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Sequence 12723, Application US/11096568A
Publication No. US20060048240A1
ABDERGL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REPERENCE: 2750-1592PUG2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 12723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIPABIRNCTELRAIYLRANYLQGGIPPGIGDLTHLTILDLSSNLLRGAIPATIGSLTHL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 RVTNNVVLEAPFL-----VGIEGSLKGSTY--NLLFCG----SCGIPVGFHLYSTHA- 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ALAALRGHFCLSSDKMVCYLLKTKAIV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 PLSSSGVSPITNNNKTSHFLNGVVIGSMSTMAIALVAVLGFL-----WVCLLSRKKNGV 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSE 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.2%; Score 86; DB 7;
21.5%; Pred. No. 1.3;
tive 23; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (1). (584)
OTHER INFORMATION: Ceres Seq. ID no. 14303176
                                                                                                                                                                                                                                                                                                                      ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 21.55
Matches 47; Conservative
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US-11-096-568A-12723
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; Sequence 12722, Application US/11096568A; Publication No. US20060048240A1; GENERAL INFORMATION: RESULT 2 US-11-096-568A-12722

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APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
SEQ ID NO:19014
LENGTH: 227
     264 PLSSSGVSPITNNNKTSHFLNGVVIGSMSTMAIALVAVLGFL-----WVCLLSRKKNGV 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----CHAQLSDAGHLSW 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 SMEWDTQVVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAW 95
                                                                                                                                                                                                                                                                                                                                            APPLICAT: Bristol-Myers Squibb Company
TITLE OP INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES
FILE REFERENCE: DOOY 2D 17/
CURRENT APPLICATION NUMBER: US/11/143,984A
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US 60/256,868
PRIOR PILING DATE: 2000-12-20
PRIOR PLING DATE: 2000-13-30
PRIOR PLING DATE: 2001-05-01
PRIOR PLING DATE: 2001-05-01
PRIOR PLING DATE: 2001-05-01
PRIOR PLING DATE: 2001-06-05
PRIOR PLING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 208
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 38
LENGTH: 1711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 7; Length 1711;
                                                                                  181 NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSE 219
                                                                                                                                  318 NYEKMDKOTVPDGAKLVTYOWNLPYSSGEIIRRLELLDE 356
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LOCATION: (122)..(122)
OTHER INFORMATION: Xaa is any aa, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-11-096-568A-19014
Sequence 19014, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
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. Sequence 38, Application US/11143984A
. Publication No. US20060014180A1
. GENERAL INFORMATION:
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NAME/KEY: misc_feature
LOCATION: (1)..(227)
OTHER INFORMATION: Ceres Seq. ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Zea mays subsp. mays
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Best Local Similarity 29.6%;
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 DLSRSLGAVVF 106
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APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE OF INVENTION: Therby
FILE REPERBNCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION NUMBER: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 12722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12721, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 ŘPLN---LSTNFFSGEIPNÝGVLGTFKSŠSÝVGNĽELCGLPIOKGČRGTLGFPAVLPHSD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----ALAALRGHFCLSSDKMVCYLLKTKAIV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 PIPABIRNCTELRAIYLRANYLQGGIPPGIGDLTHLTILDLSSNLLRGAIPATIGSLTHL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 PERCAVFOCAQCHAV-----GAVVFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 PIPABIRNCTELRAIYLRANYLQGGIPPGIGDLTHLTILDLSSNLLRGAIPATIGSLTHL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 RVTNNVVLEAPFL-----VGIEGSLKGSTY--NLLFCG-----SCGIPVGFHLYSTHA- 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 PLSSSGVSPITNNNKTSHFLNGVVIGSMSTMAIALVAVLGFL-----WVCLLSRKKNGV 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----ALAALRGHFCLSSDKMVCYLLKTKAIV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.2%; Score 86; DB 7; Length 619; Best Local Similarity 21.5%; Pred. No. 1.4; Matches 47; Conservative 23; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.2%; Score 86; DB 7; Length 644; 21.5%; Pred. No. 1.5; tive 23; Mismatches 69; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSE 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 NYEKMDKQTVPDGAKLVTYQWNLPYSSGEIIRRLELLDE 331
                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
DCATION: (1)...(619)
OTHER INFORMATION: Ceres Seq. ID no. 14303175
US-11-096-568A-12722
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: LOCATION: (1)...(644)

: OTHER INFORMATION: Ceres Seq. ID no. 14303174

US-11-096-S68A-12721
                                                                                                                                                                                                                                                                        ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 21.5
Matches 47; Conservative
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US-11-096-568A-12721
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APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptider
TITLE OF INVENTION: Therby
TITLE OF INVENTION: 176-2159-2169-2159-200-2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT PPLICATION NUMBER: US/11/096,568A
NUMBER OF SEQ ID NOS: 34471
LENGTH: 282
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APPLICANT: MASCIA, Peter
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: ALEXANDROV, Nickolai
TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
CURRENT APPLICATION NUMBER: US/11/172,740
CURRENT PILING DATE: 2005-06-30
PRIOR FILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
PRIOR PILING DATE: 2004-06-30
PRIOR PILING DATE: 2004-06-30
PRIOR PILING DATE: 2004-06-30
PRIOR PILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.6%; Score 79.5; DB 7; Length 282; Best Local Similarity 24.5%; Pred. No. 2.2; Matches 24; Conservative 11; Mismatches 40; Indels 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 SGCCXPP--TXCNFT-----YTXGTEW-TRTAAGSAP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 LQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 GNDEDDLCYGCOSCKAGVVDALKRDWKRAAIVNVVILS 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (177)..(177)
OTHER INFORMATION: Xaa is any aa, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (181)...(181)
OTHER INFORMATION: Xaa is any aa, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature
; LCCATION: (188)
.: OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-19012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (1). (282)
OTHER INFORMATION: Ceres Seq. ID no. 12368185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (1). (306)
OTHER INFORMATION: Ceres CLONE ID no. 1459706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Zea mays subsp. mays
            US20060048240A1
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SEQ ID NO 327
LENGTH: 306
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-11-172-740-327
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---AGRDCSAW 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 SRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEEPAAGPQLPSW 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 SRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEEPAAGPQLPSW 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                       6.6%; Score 79.5; DB 7; Length 227; 24.5%; Pred. No. 1.6;
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                                  NAME/KEY: misc feature
LOCATION: (126)..(126)
OTHER INFORMATION: Xaa is any aa, unknown or other
                                                                                                                                              FRATURE:
NAME/KEY: misc feature
NOCATION: (133)
COTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-19014
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LOCATION: (173)..(173)
JTHER INFORMATION: Xaa is any aa, unknown or other
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LOCATION: (177)..(177)
OTHER INFORMATION: Xaa is any aa, unknown or other
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OTHER INFORMATION: Ceres Seq. ID no. 12368186
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CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 19013
LENGTH: 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19013, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
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US-11-096-568A-19012
; Sequence 19012, Application US/11096568A
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ORGANISM: Zea mays subsp. mays
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Best Local Similarity
Matches 24; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-096-568A-19013
FEATURE:
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83 CHAVLADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCG- 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 CHAVLADSVHLAMDLSRSLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCG- 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 CYWIL-HSIAL-----YGGPTVDDELESNAI---DFLGRCQGSEGG-----YGGGPGQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                             142 IPVGFHLYSTHA---ALAALRGHFCLSS---DKMVCYLLKTK-----AIVNASEMDIQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 IDQASFITSMEWDIQ----VVKGSSPLGP--AGLGAEEPAAGPQLPSWLQPERCAVFQCAQ 82
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                                                                                                                                                                                                         28 IDQASFTTSMEWDTQ---VVKGSSPLGP--AGLGAEEPAAGPQLPSWLQPERCAVFQCAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ghassemian, Majid
APPLICANT: Cutler, Sean
APPLICANT: Donetta, Dario
IITLE OF INVENTION: Stress Tolerance and Delayed Senescence in Plants
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Wiggum gene
US-11-229-371-87
                                                                                                 Query Match 6.6%; Score 79; DB 7; Length 482; Best Local Similarity 26.3%; Pred. No. 5.1;, Matches 47; Conservative 25; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 7; Length 482;
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26.3%; Pred. No. 5.1;
tive 25; Mismatches
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CURRENT APPLICATION NUMBER: US/11/229,371
CURRENT FILING DATE: 2005-09-16
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Publication No. US20060021092A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: 60/294,766
PRIOR FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 60/348,909
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 10/210,760
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PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/191,687
PRIOR FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 178
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PRIOR FILING DATE: 2002-08-27
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PRIOR FILING DATE: 2001-08-01
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Best Local Similarity 26.3%
Matches 47; Conservative
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ORGANISM: Arabidopsis sp.
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                                                                                                                                                                                                                              LOCATION: _ _ OTHER INFORMATION: Utility: Useful for making plants with increased biomass and foli
                                                                                                                                                OTHER INFORMATION: Utility: Useful for increasing chlorophyll and photosynthetic cap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 IA-ALRGHFCLSSDKMVCYLLKTKAIV--NASEMDIONVPLSEKIAELKEKIVLTHNRLK 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 LGAVVPSRVTNNVVLEAPPLVGIEGSLKGSTYNLLFCGSCGIPVG-FHLYST-----HAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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APPLICANT: Ghasemian, Majid
APPLICANT: Cutler, Sean
APPLICANT: Cutler, Sean
APPLICANT: Bonetta, Dario
TITLE OF INVENTION: Stress Tolerance and Delayed Senescence in Plants
FILE REPERBUES: 22542-007CIP2CON1
CURRENT APPLICATION NUMBER: US/11/229,371
CURRENT FILING DATE: 2005-09-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
                                              OTHER INFORMATION: Utility: Useful for delaying flowering time
                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 6.6%; Score 79.5; DB 7; Length 306; 1 Similarity 23.7%; Pred. No. 2.4; 46; Conservative 30; Mismatches 95; Indels 23
                                                                                                                                                                                                                                                                                                                                   ; LOCATION: -
; OTHER INFORMATION: Utility: Useful for making smaller plants US-11-172-746-327
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PRIOR FILING DATE: 2002-05-31
PRIOR FILING DATE: 2001-05-31
PRIOR FILING DATE: 2001-05-31
PRIOR FILING DATE: 2001-06-31
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-09-01
PRIOR FILING DATE: 2001-09-01
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/393,96
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/39,96
PRIOR APPLICATION NUMBER: 60/39,96
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/391,687
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PRIOR FILING DATE: 2002-08-27
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APPLICATION NUMBER: 10/160,764
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ORGANISM: Unknown Organism
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SOFTWARE: PatentIn Ver. 2.1
                                                                                                 NAME/KEY: misc_feature
LOCATION:
                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
  NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
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Best Local Similarity
Matches 46; Conserva
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LENGTH: 482
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Fublication No. US20060031966A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: McCourt, Peter
APPLICANT: Glassemian, Majid
APPLICANT: Glassemian, Majid
APPLICANT: Cutler, Sean
APPLICANT: Bonetta, Dario
ITTLE OF INVENTION: Stress Tolerance and Delayed Senescence in Plants
FILE REFERENCE: 22542-007CIP2CON2
CURRENT APPLICANTON NUMBER: U5/11/228,923
CURRENT APPLICATION NUMBER: 10/229,541
PRIOR APPLICATION NUMBER: 10/129,541
PRIOR APPLICATION NUMBER: 10/160,764
PRIOR FILING DATE: 2002-08-27
PRIOR FILING DATE: 2001-05-31
PRIOR PLING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/348,909
PRIOR APPLICATION NUMBER: 60/349,909
PRIOR PLING DATE: 2001-08-01
PRIOR PLING DATE: 2001-08-01
PRIOR PLING DATE: 2001-10-22
PRIOR PLING DATE: 2001-12-04
PRIOR PLING DATE: 2001-12-04
PRIOR PLING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/39,684
PRIOR PLING DATE: 2001-12-04
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Publication No. US20060031966A1

GENERAL INFORMATION:
APPLICANT: McCourt, Peter
APPLICANT: Ghassemian, Majid
APPLICANT: Cutler, Sean
APPLICANT: Ghassemian, Pajid
APPLICANT: Grassemian, Pain
APPLICANT: Usures Tolerance and Delayed Senescence in Plants
FILE REPERDICE: 1254-007CIP2CON2
CURRENT APPLICATION NUMBER: US/11/228,923
CURRENT FILING DATE: 2005-09-16
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Best Local Similarity 26.3%; Pred. No. 5.1;
Matches 47; Conservative 25; Mismatches
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PRIOR FILING DATE: 2002-08-27
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83 CHAVLADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCG- 141
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APPLICANT: Glassemian, Majid
APPLICANT: Glassemian, Majid
APPLICANT: Glassemian, Majid
APPLICANT: Cutler, Sean
APPLICANT: Cutler, Sean
APPLICANT: Bonetta, Dario
TITLE OF INVENTION: Stress Tolerance and Delayed Senescence in Plants
FILE REFERENCE: 22542-007CIP2CON3
CURRENT APPLICATION NUMBER: 10/11/228,875
CURRENT FILING DATE: 2005-09-16
PRIOR PELING DATE: 2002-08-27
PRIOR APPLICATION NUMBER: 10/160,764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 482;
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Best Local Similarity 26.3%; Pred. No. 5.1;
Matches 47; Conservative 25; Mismatches
PRIOR APPLICATION NUMBER: 10/160,764
PRIOR PILING DATE: 2002-05-31
PRIOR PILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: 60/294,766
PRIOR PILING DATE: 2001-05-31
PRIOR PELING DATE: 2001-10-22
PRIOR PPLICATION NUMBER: 60/348,909
PRIOR PILING DATE: 2001-0-22
PRIOR APPLICATION NUMBER: 60/309,396
PRIOR PILING DATE: 2001-08-01
PRIOR PILING DATE: 2001-08-01
PRIOR PILING DATE: 2001-12-04
PRIOR PILING DATE: 2001-12-04
PRIOR PILING DATE: 1999-11-13
SROFWARRE: PATENTING NUMBER: 69/31,687
PRIOR PILING DATE: 1999-11-13
SOFTWARRE: PATENTING NUMBER: 09/191,687
PRIOR PILING DATE: 1999-11-13
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PRIOR APPLICATION NUMBER: 60/294,766
PRIOR APPLICATION NUMBER: 60/348,909
PRIOR FILING DATE: 2001-05-31
PRIOR PELLICATION NUMBER: 60/348,909
PRIOR FILING DATE: 2001-10-22
PRIOR PILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: 10/210,760
PRIOR FILING DATE: 2002-08-01
PRIOR FILING DATE: 2001-08-01
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PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 178
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 87
TYPE: PRI
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Publication No. US20060037108A1
GENERAL INFORMATION:
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; ORGANISM: Arabidopsis sp.
US-11-228-923-177
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155 LP---HLATTYAAVNALVTLGGDKALSSINREKMSCFLRRMKDTSGGFRMHDMGEMDVR 210
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APPLICANT: Cutler, Sean
APPLICANT: Cutler, Sean
APPLICANT: Boneta, Dario
TITLE OF INVENTION: Stress Tolerance and Delayed Senescence in Plants
FILE REFERENCE: 22542-007CIP2CON3
CURRENT APPLICATION NUMBER: US/11/228,875
CURRENT FILING DATE: 2005-09-16
                                   ; OTHER INFORMATION: Description of Unknown Organism: Wiggum gene
US-11-228-875-87
                                                                                              Query Match 6.6%; Score 79; DB 7; Length 482; Best Local Similarity 26.3%; Pred. No. 5.1; Matches 47; Conservative 25; Mismatches 49; Indels
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26.3%; Pred. No.
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R FILING DATE: 2002-08-27

R FILING DATE: 2002-05-31

R APPLICATION NUMBER: 60/294,766

R FILING DATE: 2001-05-31

R APPLICATION NUMBER: 60/348,909

R FILING DATE: 2001-10-22

R RAPLICATION NUMBER: 10/210,760
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APPLICATION NUMBER: 60/309,396
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APPLICATION NUMBER: 60/337,084
ORGANISM: Unknown Organism PEATURE:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30; Indels 30; Gaps
                                                                           APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES
FILE REFERENCE: D0072 DIV1
CURRENT APPLICATION NUMBER: US/11/143,984A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.6%; Score 79; DB 7; Length 1705; Best Local Similarity 25.2%; Pred. No. 28; Matches 26; Conservative 17; Mismatches 30; Indels
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                                                                                                                                                                                                                   CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US 60/256,868
PRIOR FILING DATE: 2000-12-20
PRIOR PILING DATE: 2000-13-0
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-05-01
PRIOR PELICATION NUMBER: US 60/287,735
PRIOR PILING DATE: 2001-06-05
PRIOR PILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR PILING DATE: 2001-06-05
SOFTWARE: PATCHING DATE: 2001-06-25
SOFTWARE: PATCHING DATE: 2001-06-25
SOFTWARE: PATCHIN VERSION 3.2
SEQ ID NO 3.7
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Job time : 25 secs
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Sequence 37, Application US/11143984A Publication No. US20060014180A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus musculus US-11-143-984A-37
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